

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n-model

Run on: March 14, 2006, 07:44:42 ; Search time 15376 Seconds
(without alignments)
4898.385 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6787

Sequence: 1 MLPVQVEKPNLQDANLCS.....MTVNTSNGSPSTLTFETAL 1325

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database :

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6: gb_pat:.*
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13: gb_vl:.*
14: gb_hlg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6787	100.0	4004	8	AY207008 Homo sapi
2	6779	99.9	4231	6	AR589389 Sequence
3	6779	99.9	4231	6	AX210645 Sequence

4	6779	99.9	4231	6	AX686744 Sequence
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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
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AY207008	AY207008	Homo sapiens ATP-binding cassette transporter C4 (ABCC4) mRNA, complete cds.	AY207008	AY207008	AY207008.1 GI:31322320	Homo sapiens (human)	1	Kato, R. and Ishikawa, T.	Submitted (24-DEC-2002)	Department of Biomolecular Engineering, Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, 4259 Nagatsuta-cho, Midori-ku, Yokohama-shi, Kanagawa 226-8501, Japan	1..4004 Location/Qualifiers 1..4004 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cfeature_type="kidney" 1..4004

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ORIGIN

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Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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US-09-976-858-42 (1-1325) x AY207008 (1-4004)

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RESULT 2
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LOCUS Sequence 1 from patent US 6803184.
DEFINITION AR589389
ACCESSION AR589389
VERSION AR589389.1 GI:56636669
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4231)
AUTHORS Krush, G. and Lee, K.
TITLE MPR-related ABC transporter encoding nucleic acids and methods of use thereof
JOURNAL Patent: US 6803184-A 1 12-OCT-2004;
Fox Chase Cancer Center: Philadelphia, PA
FEATURES
source Location/Qualifiers
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Best Local Similarity: 99.8% Mismatches: 1
Query Match: 99.9% Indels: 0
Gaps: 0
US-09-976-858-42 (1-1325) x AR589389 (1-4231)

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Db 116 ATGCTGCCCTGTACAGAGAGGTGAAGCCCAACCCGCTCAGAGACCGCAACATCTGCTCA 175
Qy 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGln 40
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Qy 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
Db 236 GAGAGATGATATATTCACTGCTGCGCAGAGACCGCTCAGACCACTTGGAGAGGAGTG 295
Qy 61 GlnGlyPheTyrAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
Db 296 CAGGGCTTGGGATTAAGAAAGTTTAAAGCTGAGAAATGACGACAGAAAGCCCTTCTTA 355
Qy 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyLysPheThrLeu 100
Db 356 ACAAGAGCAATCATAAAGTTTAACTGGAATCTTAATTAGTTTGGGAATTTTACGTTA 415
Qy 101 IleGluGluSerAlaLysValIleGlnProLysPheLeuGlyLysIleIleAsnTyrPhe 120

Db 416 ATTGAGAAAGTCCAAAGTAAATCCAGCCCATATTTTGGAAAAATTAATTATTTT 475
Qy 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
Db 476 GAAATTTATGATCCATGGAATTTCTGGCTTTGAACACAGGGTACGCCATATCCAGGG 535
Qy 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
Db 536 CTGACTTTTGGACCCCTCATTTTGGCTATACGATCACTTAATTTTATCCATCGTCA 595
Qy 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
Db 596 TGTGCTGGAGTGAAGTTTACAGATACCATATGATGATTTATTCGAAAGCACTTCGT 655
Qy 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
Db 656 CTTAATTACATGGCCATGGGGAAGCAACACAGGCCAGATGATCATCTGCTGCTCAAT 715
Qy 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
Db 716 GATGTGAACAAATTGATCAGGTGACAGTGTCTTACACTTCTGTGGGACAGCACTG 775
Qy 221 GlnAlaIleAlaValThrAlaLeuLeuThrPheGluIleGlyLysSerCysLeuAlaGly 240
Db 776 CAGGCGATGCGAGTACCTGCTCTGATGAGATGAGATATCTGTCCTGCTGG 835
Qy 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
Db 836 ATGGCATTTCTAATCATTTCTGCTGCTTGGCAAACTGTTTGGAGATTGTTCTCATCA 895
Qy 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Qy 281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Qy 301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320
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Qy 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
Db 1076 TTGGCTTGTGTTTTCAGTCAAGCAAAATCATCGTTTGGACCTTACCACTACGTCG 1135
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Qy 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
Db 1256 GTCAACATCCGAAGATCAGACCTTTTGTACTGTGATGATTCACAGGCAACCGT 1315
Qy 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
Db 1316 CAGCTGCCGTCAAGTGTAAAGATGTGATGTCAGAGATTTCATGCTTTTGGAGT 1375
Qy 421 LysAlaSerGluThrProThrLeuGlnLysLeuSerPheThrValArgProGlyGluLeu 440
Db 1376 AAGGATCAGAGACCCCAACTCTACAAAGCTTCTTACGTGACAGCTGCGCAATTG 1435
Qy 441 LeuAlaValIleGlyProValIleValaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
Db 1436 TTAGCTGTGTGCGGCCCGTGGAGACAGGAAGTATCATCTGTAAAGTCCGCTCGGG 1495
Qy 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgGlyIleAlaTyrValSerGln 480
Db 1496 GAATTGGCCCAAGTCAAGGCGTGTGACGCTGATGAGAAAGATTGCCATGTGTCTCAG 1555

Qy	481	GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyValPheTyrGlu	500
Db	1556	CAGCCCTGGGGTCTCGGGAACCTCGAGGAGTAATTTATTTGGGAATAATGA	1615
Qy	501	LygIuNrGTYrGluYValIleIyValaCYaIaLeuYslyAspLeuGlnLeu	520
Db	1616	AAGAAAGCATATGAAAAAGCATATAAGCTTGCTGTAAGAAAGATTACAGCTGTG	1675
Qy	521	GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGln	540
Db	1676	GAGATGGTGAATCTGACTGTATGAGAGATCGGGAAACCAAGCTGAGTGGGCA	1735
Qy	541	AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuAspAsp	560
Db	1736	GCAGGGGTAACTTTCGAAAGACAGTGATCAAGATGTGCATCTATCTCTCGAAGAT	1795
Qy	561	ProLeuSerAlaValAspAlaGlyValSerArgHisLeuPheGlnLeuCysGln	580
Db	1796	CCTCACTGAGATGATGATCGGAAGTTAGCAACCTTGTCGAACGTGTATTGTCAA	1855
Qy	581	IleLeuHisGluYsIleThrIleLeuValThrHisGlnLeuGlnTyrLeuYsAlaAla	600
Db	1856	ATTTTGCATGAGGAAGATACAAATTTAGTACTCATCAGTTGCAGTACCTAAAGCTGCA	1915
Qy	601	SerGlnIleLeuIleLeuYsAspGlyValMetValGlnYsGlyThrTyrThrGluPhe	620
Db	1916	AGTCAGATTCGATTAATGAAAGATGGTAAATGCTGCAGAAAGGAGCACTTACATG	1975
Qy	621	LeuYsSerGlyIleAspPheGlySerLeuLeuYslyAspAsnGluSerGluGln	640
Db	1976	CTAAATCTGGTAAATGATTTTGGCTCCCTTTTAAAGAGTAATGAGAAAGTAA	2035
Qy	641	ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTyr	660
Db	2036	CCTCAAGTCCAGGAATCTCCACACATAAGAAATGTACTTCTCAGAGCTTCGAGTTG	2095
Qy	661	SerGlnGlnSerSerArgProSerLeuYsAspGlyAlaLeuGlnSerGlnAspThrGlu	680
Db	2096	TCTCAACATCTTCTTAAGCCTCTCTTGAAGAATGATGTGCTCGAGAGCAAGATACAG	2155
Qy	681	AsnValProValThrLeuSerGluGluAsnArgSerGluGlyValPheValGlyPheGlnAla	700
Db	2156	AATGTCCAGATTAACATACATCAGAGAGAACCGTGTCTGAAGAAAAGTTGGTTTCAGGCC	2215
Qy	701	TyrIysAsnTyrPheArgAlaGlyAlaHisArgIleValPheIlePheLeuIleLeuLeu	720
Db	2216	TATTAAGATTAATCTCAGAGCTGGTGCTCAGTGAATGTCTCATTTCTTATCTCTCTA	2275
Qy	721	AsnThrAlaAlaGlnValAlaTyrValIleGlnAspTrpTrpLeuSerTyrTrpAlaAsn	740
Db	2276	AACACTGAGCTCAGGTGGCTATGTGCTTCAAGATTGTGTGCTTCACTGGGCAAC	2335
Qy	741	LygGlnSerMetLeuAsnValThrValAsnGlyGlyIyAsnValThrGluYsLeuAsp	760
Db	2336	AAACAAGTATGCTTAATATGCTACGTAAATGAGAGAGAAATGTAAACCGAAGAACTGAT	2395
Qy	761	LeuAsnTrpTyrIleGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle	780
Db	2396	CTTAACCTGTAATCTTAAGAAATTTATTCAGGTTTAACTGATGCTACCGTCTTTTGGCATA	2455
Qy	781	AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnYs	800
Db	2456	GCAAGATCTCATTTGGTATTTCTACGCTCTTGTAACTTTCACAACTTTCACAACTTTC	2515
Qy	801	MetPheGlnSerIleLeuYsAlaProValLeuPheAspArgAsnProIleGlyArg	820
Db	2516	ATGTTTGAAGTCAATTCGAAAGCTCCGGTATTAATCTTTGATAGAATCCAAATGAGAGA	2575
Qy	821	IleLeuAsnArgPheSerIyAspIleGlyHisIleuAspAspLeuLeuProLeuThrPhe	840
Db	2576	ATTTTAAATCGTTTCTCCAAAGAACATTTGGACATGTGATGATTTTGCCCGCTACAGTTT	2635

OY		841	LeuAspPheIleGIInThrLeuGlnValValGlyValValSerValAlaValAlaValAl	860
Dd		2636	TTCATATTTCATCCAGACATTGCCTAACAGTGGTGGTGGTCTCTGGCGCTGGGCCGTG	2695
OY		861	IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg	880
Dd		2696	ATTCCTTGGAATCGGAATACCCTTGTTGCCCTTGGAATCATTTTTCATTTTTCTTCGGCGA	2755
OY		881	TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal	900
Dd		2756	TATTTTTTGGAAACGTCMAAGAGATGTGAACGGCCTGGAACTCAACTCCGAGCTCCAGTG	2815
OY		901	PheSerHisLeuSerSerSerLeuGlnGlyLeuThrPrhTrIleArgAlaTyrLysAlaGlu	920
Dd		2816	TTTTCCCATCTGTCATCTTCTCTCCAGGGGCTCTGGACCAATCCGGGATACCAAGCAAA	2875
OY		921	GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeu	940
Dd		2876	GAGAGGTGTCCAGAACCTGTTGATGCACACAGGATTTACATTCAAGGCGTTGGTCTTG	2935
OY		941	PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal	960
Dd		2936	TTTTTTCACAACGTCGCCCTGGTGGCGGTCCGTCTGGATGCCATCTGGCCATGTTTGTGC	2995
OY		961	IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly	980
Dd		2996	ATCATCTGTGCTTTGGGTCCCTGATTTCTGGCAAAACTGTGATGCCGGGACAGTTGGT	3055
OY		981	LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer	1000
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OY		1001	AlaGluValGluAsnMetIleSerValGluArgValIleGluTyrThrAspLeuGlu	1020
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OY		1021	LysGluAlaProTrpGluTyrGlnLysArgProProAlaTrpProHisGluGlyVal	1040
Dd		3176	AATAAACAACCTTGGGAATATCAAGAAAGCCCAACACAGCCTGGCCCCCATGAAGAGTGT	3235
OY		1041	IleIlePheAspAsnValaAsnPheMetTyrSerProGlyGlyProLeuValIleuLysHis	1060
Dd		3236	ATATCTTTTGCATATGGAATCTCATATACAGTCCAGATGGGCGCTCTGGATCTGAACAT	3295
OY		1061	LeuThrAlaLeuIleLysSerGlnLysValGlyLysValGlyArgThrGlyAlaGly	1080
Dd		3296	CTGACACACCTCATTAATACAAAGAAAGTTGGCATTTGGGAAACCGGAGCTCGA	3355
OY		1081	LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle	1100
Dd		3356	AAAAGTTCCCTCATCTCAGCCCTTTTAGATTGTCAGAACCCGAAAGGTAAATTTGGATT	3415
OY		1101	AspLysIleIleuThrTrhGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle	1120
Dd		3416	GATTAAGATCTTTGACAACTGAATTTGACCTTCACATTTAAGAAAGAAATGTCATATATA	3475
OY		1121	ProGlnGluProValIleuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu	1140
Dd		3476	CCTCAGAACCTGTTTGTTCATCTGGAACAATAGGAAAAAACCCTGATCCCTTTAAGAG	3535
OY		1141	HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu	1160
Dd		3536	CACACGGATGAGGAACGTGGAAAGCCTTCAAAGAGGTACAACTTAAAGAAACCATTTGAA	3595
OY		1161	AspLeuProGlyLysMetLaaPrhTrhGluLeuAlaGluSerCylSerAsnPheSerValGly	1180
Dd		3596	GATCTTCTCGGTAAAGATACGAATTAGCAGAAACAGAGATCCAATTTTAGTGTGGA	3655
OY		1181	GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle	1200
Dd		3656	CNAAGACAACCTGGGTGTGCTTGGCCAGGGGCAATTTCTCAGAAAAATCGAATTTGATTAT	3715
OY		1201	AspGluAlaThrAlaAsnValaAspProArgThrAspGluLeuIleGlnLysLysIleArg	1220

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Db      3716 GATGAGACGACGCAAAATGTGATCCAAAGCTGATTAATACAAAAAAATCCCG 3775
Oy      1221 GtUvsPheAlAHiscYsthrValLeuThrIleAlaHicArgLeuAnthrIleIleAep 1240
Db      3776 GAGAAATTTGGCCCATCGACCGCTGCTACCAATTGCACAGATTGAAACCACTTATTGAC 3835
Oy      1241 SerAspLysIleMetValIleuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
Db      3836 AGCGACCAAGATATAGTTTATGATTTCAGGAAGACTGAAGAATATGATGACCGATGTT 3895
Oy      1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
Db      3896 TTGCTGCGCAAAATGAAAGAGCCCTATTATTCAAGATGTGTCAACACCTGGGCAAGCGA 3955
Oy      1281 AlaAlaIleuThrcGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
Db      3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGTACTTCMAAGAAATTAATCCACTATT 4015
Oy      1301 GtYHicsthrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
Db      4016 GGTCACTGACGACCACTGGTTTAAACACTTCCAAATGACAGCCCTGACCTTAATTAT 4075
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RESULT 3
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LOCUS      AX210645 4231 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 287 from Patent WO0157058.
ACCESSION  AX210645
VERSION     AX210645.1 GI:15424905
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE   1
AUTHORS     Rosenthal, A., Hinzmann, B., Schaefer, R., Zuber, J., Tcherntseva, O.,
Grips, M., Hellriegel, M., Schmitz, A.C. and Sers, C.
TITLE       Detection of differential gene expression
JOURNAL     Patent: WO 0157058-A 287 09-AUG-2001;
Metagen Gesellschaft fuer Genomforschung mbH (DE)
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             /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 4231
Score: 6779.00 Matches: 1323
Percent Similarity: 99.9% Conservative: 1
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 99.9% Indels: 0
DB: 6 Gaps: 0

US-09-976-858-42 (1-1325) x AX210645 (1-4231)
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Db      116 ATGCTCCCGCTGTAACAAGAGGTGAAGCCCAACCCGCTGACGACCGCAACATCTCTCA 175
Oy      21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGln 40
Db      176 CGGCTGTTCTTCTGGTGGCTCAATCCCTGTTAAATTGGCCATTAACGAGATTAGAG 235
Oy      41 GluAspAspMetTyrSerValLeuProGlnAspArgSerGlnHisLeuGlyGluGluLeu 60
Db      236 GAAGATGATATATATTCACTGCTGCGAAGACCGCTCAACGACCTTGAGAGAGATTG 295

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Oy      61 GlnGlyPheTrpAspLysGluValIleuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Oy      81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValIleGlyIlePheThrLeu 100
Db      356 ACMAAGACAAATCAATAAAGTTACTGGAATCTTATTTAGTTTGGAAATTTTAACGTTA 415
Oy      101 IleGlnIleSerAlaLysValIleGlnProIlePheLeuGlyLysIleLeuAsnTyrPhe 120
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Oy      141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
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Oy      181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuSerAsn 200
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Oy      321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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OY	461	GluLeuAlaProSer	ThiLeuValSerValHisGlyArgIleAlaTyrValSerGln	480	
Db	1496	GAAATTGGGCC	CCCAAGTCAGGGGCTGGTCAAGCGTGCATGAGAAATTCCTATGTGTCCAG	1555	
OY	481	GlnProTyrVal	PhaSerGlyThrLeuArgSerAsnIleLeuPheGlyValLeuTyrGlu	500	
Db	1556	CAGCCCTGGGCTG	CTCCGGAACTCTGAGAGACTAATATTATTGGGAAGAAATATGAA	1611	
OY	501	LYSGIUA	RGTYRGluLeuValIleLeuValaCysValaLeuLeuValaAspLeuIleuLeu	520	
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OY	521	GluAspGlyAsp	LeuThrValIleGlyAspArgGlyThrThriLeuSerGlyGlnGlyAs	540	
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OY	541	AlaArgValaAsn	LeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp	560	
Db	1736	GCAACGGGTAA	ACCTTGCAAGACAGATGTACAAGATGTGACATCATCTCTCGACAGAT	1799	
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Db	1856	ATTTTGCATG	AGAAATACATCATTTTATAGACTCATCTGACTTCAGATCACTCAAGCTGCA	1911	
OY	601	SerGlnIleLeu	IleLeuIleAspGlyLeuSerValaGlnLeuGlyThrTyrThriGluPhe	620	
Db	1916	AGTCAGATTCT	GAATTTTGAAAGATGGTAAATGGTCAGAAAGGGACTTACACTGAGTTC	1972	
OY	621	LeuIleSerGly	IleAspPheGlySerLeuLeuValblyAspAsnGluGluSerGluGln	640	
Db	1976	CTAAATCTG	GTATGATTTTGGCTCCCTTTTAAAGAAAGATTAAGAGAAAGTGAACA	2033	
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OY	661	SerGlnGlnSer	SerArgProSerLeuIleAspGlyAlaLeuGluSerGlnAspThriGlu	680	
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OY	701	TyrIleuAsnTyr	PhaArgAlaGlyAlaHisTyrIleValaPheIlePheLeuIleLeuLeu	720	
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OY	721	AsnThrAlaAla	GlnValaAlaTyrValaLeuGlnAspTyrTyrPheLeuSerTyrTyrAlaAsn	740	
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Homnidae; Homo.
REFERENCE
AUTHORS Eulenberger, K., Broemner, G., Ciossek, T., Haeder, T., and Steuernagel, A.
TITLE Protein disulfide isomerase and ABC transporter homologous proteins
JOURNAL involved in the regulation of energy homeostasis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Lee,K., Belinsky,M.G., Bell,D.W., Teesta,J.R. and Krub,G.D.
TITLE Isolation of MOAT-B, a widely expressed multidrug
resistance-associated protein/canalicular multispecific organic
anion transporter-related transporter
Cancer Res. 58 (13), 2741-2747 (1998)
JOURNAL
PUBMED 9661885
REFERENCE 2 (bases 1 to 4231)
AUTHORS Lee,K., Belinsky,M.G., Bell,D.W., Teesta,J.R. and Krub,G.D.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1998) Medical Oncology, Fox Chase Cancer Center,
7701 Burholme Ave., Philadelphia, PA 19111, USA
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Homnidae; Homo.
REFERENCE 1

AUTHORS

Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A.,
Beckmann, G., Brumendorf, T., Kimmann, H., Roepcke, S., Hermann, K.,
Kinzhong, L., Pilsarsky, C. and Staub, E.
Human nucleic acid sequences obtained from prostatic carcinomas
Patent: WO 2004/076614-A 115 10-SEP-2004;

JOURNAL

Hinzmann, Bernd (DB); Dahl, Edgar (DB); Rosenthal, Andre (DB);
Specht, Thomas (DB); Schmitt, Armin (DB)

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 Homnidae; Homo.
 REFERENCE
 AUTHORS
 1 Francis-Lang, H., Winter, C.G., Ventura, R.B., Bjerke, L.M.,
 Lickteig, K., Adamkewicz, J.I., Zhang, H. and Hal, B.
 Modcats as modifiers of the beta-catenin pathway and methods of use
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 JOURNAL
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 US-09-976-858-42 (1-1325) x CS038316 (1-5871)

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 LOCUS Sequence 24177 from Patent WO0160860.
 DEFINITION CQ492310
 ACCESSION CQ492310.1 GI:41457929

KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 Schlegel,R., Endege,W.O. and Monahan,J.B.
 TITLE Genes differentially expressed in human prostate cancer and their
 use

JOURNAL Patent: WO 0160860-A 24177 23-AUG-2001;
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 1. 4515
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 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 4515
 Score: 6770.00 Matches: 1324
 Percent Similarity: 99.88 Conservative: 0
 Best Local Similarity: 99.88 Mismatches: 1
 Query Match: 99.74 Indels: 1
 DB: 6 Gaps: 0

US-09-976-858-42 (1-1325) x CQ492310 (1-4515)

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 REFERENCE
 1 Schlegel,R., Endege,W.O. and Monahan,J.E.
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 REFERENCE
 AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
 TITLE Genes differentially expressed in human prostate cancer and their
 use
 JOURNAL Patent: WO 0160860-A 26500 23-AUG-2001;
 Millennium Predictive Medicine, Inc. (US)

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QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyValSerGln 480
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 ACCESSION CQ496370.1 GI:41461989
 VERSION CQ496370.1
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.B.
 TITLE Genes differentially expressed in human prostate cancer and their
 use
 JOURNAL Patent: WO 0160860-A 28237 23-AUG-2001;
 Millennium Predictive Medicine, Inc. (US)
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 Best Local Similarity: 99.8% Mismatches: 1
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 Hominoidea; Homo.
 1 (bases 1 to 5759)
 Adachi, M., Sampath, J., Ian, L. B., Sun, D., Hargrove, P., Flatley, R.,
 Tatum, A., Edwards, M. Z., Wezeman, M., Matherly, L., Drake, R. and
 Schuetz, J.
 Expression of MRP4 Confers Resistance to Ganciclovir and
 Compresses Bystander Cell Killing
 J. Biol. Chem. 277 (41), 38998-39004 (2002)
 2 (bases 1 to 5759)
 Adachi, M., Sampath, J., Sun, D. and Schuetz, J. D.
 Direct Submission
 Submitted (22-FEB-2002) Pharmaceutical Sciences, St. Jude
 Children's Research Hospital, 332 North Lauderdale St., Memphis, TN
 38105-2794, USA
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US-09-976-858-42 (1-1325) x AY081219 (1-5759)

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 REFERENCES
 1 (bases 1 to 6082)
 Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
 Kalos M.D., Fanger G.R., Retter M.W., Stolk J.A., Day C.H.,
 Vedick T.S., Carter D., Li S.X., Wang A., Skeiky Y.A.W.,

TITLE HepJr, W.T. and Henderson, R.A.
 Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: US 6512094-A 535 28-JAN-2003;
 Corixa Corporation; Seattle, WA

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US-09-976-858-42 (1-1325) x AR278592 (1-6082)

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 DB 666 TGTGCTGGAGATGAGTTACAGATGACCATGTGCCATATGATTTATGGAAGGCACTTC 725
 QY 181 LeuSerAsnMetAlaMetGlyLysThrTrpThrGlnIleValAsnLeuSerAsn 200
 DB 726 CTTAGTAACATGGCCATGGGAAAGAACACACAGGCGCATATGATCTGCTGCAT 785
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisIlePheLeuTrpAlaGlyProLeu 220
 DB 786 GATGTGAACAAGTTTATCATCGTACAGTCTTCTTACACTTCTGTGGGAGGACCACTG 845
 QY 221 GlnAlaIleLeuAlaValThrAlaLeuLeuTyrPheGlnIleGlyLysSerCysLeuAlaGly 240
 DB 846 CAGGCGATGCGACATGCTGCCCTACTCTGGATGAGATAGGAATATCGTGCCTTGGCTGG 905
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
 DB 906 ATGCAAGTTCTATATCATCTCCGCGCTTGCAAGAGCTGTTTGGGAAAGTTGTTCTATCA 965

QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleLeuGlnMetAsnGluValIle 280
 DB 966 CTGAGAGTAAATAACGCAACTTTTCAACGATGCGAGATGAGGACCATGAAATGATTTATA 1025
 QY 281 ThrGlyIleArgIleIleIleLysMetTyrAlaTyrGlyLysSerPheSerAsnLeuIleThr 300
 DB 1026 ACTGATTAAGATATATTAATAATGTACCTGGGAAAGTCAATTTTCAATTTTATACC 1085
 QY 301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
 DB 1086 AATTTGAAAGAAAGAGAGATTTTCCAGATTTCTGAGAAATTCCTGCTCAGGGGATGAT 1145
 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
 DB 1146 TTGGCTTGTTTTCAGTGCAGCAAAATCACTCGGTGTGACCTTCAACCACTTACG 1205
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyVal 360
 DB 1206 CTCTCGGCGATGTATCAACGACCGCGTGTTCGTGGAGTACCGCTGTATGGGCT 1265
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
 DB 1266 GTGGCGGTGACCGTTACCTCTTCTTCCCTAGCCATTTGAGAGGGGTGACAGGCAATC 1325
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
 DB 1326 GTCAACATCCGAAGATCCAGACTTTTGTGCTACTGTATGAGATATCAACGCGCAACGT 1385
 QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
 DB 1386 CAGCTGCGTCAGATGTAAAGATGGTCAATGTGCAGAGATTACTGCTTTTGGGAT 1445
 QY 421 LysAlaSerGluThrProThrLeuGlnLysLeuSerPheThrValArgProGlyGluLeu 440
 DB 1446 AAGCATCAGAGAACCCCAACTATACAGGCCCTTCTTACTGTCAGACCTGGCAATGG 1505
 QY 441 LeuAlaValAlaGlyProValGlyValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
 DB 1506 TTAGCTGTGTGTGGCCCGTGGAGCAGGGAATCATCATCTGTAAAGTCCCTGTGCGG 1565
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
 DB 1566 GAATTTGGCCCCAAGTACAGGCTGTGTCAGCGTCAAGAAATGCTTATGTGCTCAG 1625
 QY 481 GlnProTyrValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500
 DB 1626 CAGCCCTGGGTGTTCTCGGAACTCTGAGAGTAAATTTTATTTGGGAAGAAATACGA 1685
 QY 501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 DB 1686 AAGGAACGATATGAAAAAGTCAATAAGGCTTGTGCTCGAAMAAAGATTTTACAGCTGTG 1745
 QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
 DB 1746 GAGGATGTGATCTGACTGTGATAGAGATCGGGAAACCACTGATGTGAGAGGAGANA 1805
 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
 DB 1806 GCAAGGCTAACTCTTGCAGAGACAGCATGTATCAAGATGCTGATCTATCTCTGAGCAT 1865
 QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuLysCysGln 580
 DB 1866 CCTCTCAGTGCAGTATGATCGGAGATGTGCAACACTTGTGTGAACCTGTGTATTTGTCA 1925
 QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaIle 600
 DB 1926 ATTTTGCATGAAGAAATCAAAATTTAGTACTCATAGTTTCAAGTCACTCAAGCTGCA 1985
 QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
 DB 1986 AGTCAGATTCTGATTTGAAAGATGTGTAATAATGTGCAAGAGGACCTTACACTAGTTC 2045
 QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGlnSerGluGln 640

Db 2046 CTAATATCGTATGATTTGGCTCCCTTTAAAGAGATATAGGAAAGTGAACA 2105
 Qy 641 ProProValProGlyThrProThreuleuAmaagthPheserGlyUseterValTTP 660
 Db 2106 CCTCAAGTTCAGGAACCTCCCACTAAGAAATCGTACCTTCTCAGAGCTTCGGTTGG 2165
 Qy 661 SerGlnGlnSerSerArgProSerleuYsaapGlyAlaLeuGlnSerGlnApthGlu 680
 Db 2166 TCTCAACAACTTCTAGACCTCTTGAAAGATGGTCTCTGAGAGCCAAATACAGAG 2225
 Qy 681 AsnValProValThreuleuSerGlnGlnAmaargSerGlnGlyValGlyPheGlnAla 700
 Db 2226 AATGTCACAGTACCTATCAAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTCAGGCG 2285
 Qy 701 TyrIleAsnThrPheargAlaGlyAlaHisTTPIleValPheIlePheleuIleleu 720
 Db 2286 TATAAGATTTACTTCAAGAGCTGGTCTCACTGATTTCTCATTTTCTTATTTCTCTCA 2345
 Qy 721 AsnThrAlaAlaGlnValAlaTyrValleuGlnAapTTPleuSerTyrTrpAlaAsn 740
 Db 2346 AACCTGACGCTCAGGTTGCTTATGATGCTTCAAGATGGTGCTTTCATACCTGGGCAAC 2405
 Qy 741 LysGlnSerMetLeuAsnValThrValAenglyGlyGlyAsnValThrGluLysleuAsp 760
 Db 2406 AAACAAGATCTAAATGCTCACTGMAATGAGAGGAAATGTAAACGAGAACTAGAT 2465
 Qy 761 LeuAsnTTPYrleuGlyIleTyrSerGlyleuThrValAlaThrValleuPheGlyIle 780
 Db 2466 CTTAATCGTATCTGGAATTTATTCAGGTTTAACTGTAGTACCGTCTTTTGGCAATA 2525
 Qy 781 AlaargSerleuLeuValPheTyrValleuValAanserSerGlnThreuleuIleAsnLys 800
 Db 2526 GCAAAATCTCTATGATGATTTACGCTCTGTAACTCTTCACAAACTTGAACAACAA 2585
 Qy 801 MetPheGlnSerIleleuLysAlaProValleuPheAspArgAsnProIleGlyArg 820
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 Qy 821 IleleuAmaargPheSerIleYsaapIleGlyHisleuAspAspLeuProleuThrPhe 840
 Db 2646 ATTTTAAATCGTCTTCTCCAAAGACATGAGCACTTGATGATTTGCTGCGCGTGAAGT 2705
 Qy 841 LeuAspPheIleGlnThreuleuGlnValValGlyValAlaSerValAlaValAlaVal 860
 Db 2706 TTAGATTCATCAACAACATGCTACAGAGTGGTGGTCTCTGAGCTGTGGCGG 2765
 Qy 861 IleProTTPIleAlaIleProleuValProleuGlyIleIlePheIlePheleuArg 880
 Db 2766 ATTCCTTGATCGCAATACCTTGGTCTCCCTTGGAATCATTTTCTTGGGCA 2825
 Qy 881 TyrPheleuGlnThrSerArgAspVallyAsargleuGlnSerThrThrArgSerProVal 900
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 Qy 901 PheSerHisleuSerSerSerleuGlnGlyleuTTPThrIleArgAlaTyrIleValGlu 920
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 Qy 921 GluArgCysGlnGlnleuPheAspAlaHisGlnAspLeuHisSerGlnAlaTTPPheleu 940
 Db 2946 GAGAGTGTCAAGAACTGTTGATGCAACAGATTTTACATTCAGAGGCTTGGTTCTTG 3005
 Qy 941 PheleuThrThrSerArgTTPheAlaValAlaArgleuAspAlaIleCysAlaMetPheVal 960
 Db 3006 TTTTTCACAACGCTCCGCTGGTCCGCTCGCTGAGATGCATCTGTCCATGTTTGTGC 3065
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 Qy 981 LeuAlaLeuSerTyrAlaLeuThrleuMetGlyMetPheGlnTTPCysValAlaArgGlnSer 1000

Db 3126 TTGGCACTGCTCATGCCCCCTCAGCTCATGGGAGATTTCAAGTGTGTTCAGCAAAAGT 3185
 Qy 1001 AlaGlnValGlnAanserMetIleSerValGlnArgValIleGlnTyrThrAspLeuGln 1020
 Db 3186 GCTGAAGTGGAAATATATATATATATCTCAGTAAAGGGGCTATTAATATACAGACCTTGA 3245
 Qy 1021 LysGlnAlaProTTPGlnTyrGlnLysArgProProAlaTTPProHisGlnGlyVal 1040
 Db 3246 AAAGAGCACTTGGGAATATCAGAAACGCCCAACCAAGCTGGCCCCATGAAGAGTG 3305
 Qy 1041 IleIlePheAspAsnValAsnPhemetYrSerProGlyGlyProleuValleuLysHis 1060
 Db 3306 ATAACTTTGACAAATGTGAATCTTCAATGACAGTCCAGGCTGGGCTCTGTGATCAAGCAT 3365
 Qy 1061 LeuThrAlaLeuIleLysSerGlnGlnLysArgValGlyIleValGlyArgThrGlyValGly 1080
 Db 3366 CTGACAGCACTTAAATTAATCAAGAAAGGTTGGCATTTGGAGAAAGAACCGAGACTGGA 3425
 Qy 1081 LysSerSerleuIleSerAlaLeuPheArgleuSerGlnProGlnGlyLysIleTTPIle 1100
 Db 3426 AAAAGTTCCTCATCTCAGCCCTTTTGTGATGTCAGAACCCGAAAGTAAATTTGGATT 3485
 Qy 1101 AspLysIleleuThrThrGlnIleGlyleuHisAspLeuArglyLysMetSerIleIle 1120
 Db 3486 GATAAGATCTTGACAACTGAATTTGCACTTCAACGATTTAAAGAAAGAAATGTCATCATTA 3545
 Qy 1121 ProGlnGlnProValleuPheThrGlyThrMetArglyAsnleuAspProPheGlnGlu 1140
 Db 3546 CCTCAGGAACCTGTTTGTTCATCTGGAACAATGAGAAAGAAACCTGATCCCTTATATGAG 3605
 Qy 1141 HisThrAspGlnGlnleuTTPAsnAlaLeuGlnGlnValGlnleuGlyIleThrIleGlu 1160
 Db 3606 CACAGGATGAGAACTGTGAATGCTTCAAGAGGTACCACTTAAAGAAACCTTGA 3665
 Qy 1161 AspLeuProGlyLysMetAspThrGlnleuAlaGlnSerGlySerAsnPheserValGly 1180
 Db 3666 GATCTTCTGGTAAATGATGATCTGAATTAAGAGAAATCAGATTCATTTATGTGGA 3725
 Qy 1181 GlnArgGlnleuValCysleuAlaArgAlaIleleuAlaGlyAsnGlnIleleuIleIle 1200
 Db 3726 CAAGACAACTGGTGTGCTTCCAGGGCAATTCAGAGAAAGAAATCAATATGATTTAT 3785
 Qy 1201 AspGlnAlaThrAlaAsnValAspProArgThrAspGlnleuIleGlnLysLysIleArg 1220
 Db 3786 GATGAAGCAGCGCAATGTGATTCAGAACTGATGATTAATCAAAAAAATC-CGG 3844
 Qy 1221 GluYsaPheAlaHisCysThrValleuThrIleAlaHisArgleuAsnThrIleleuAsp 1240
 Db 3845 GAGAAATTTGCCCACTGACCGGTGTACATTTGACACAGATTTGAACACCATTTATGAC 3904
 Qy 1241 SerAspLysIleMetValleuAspSerGlyArgleuLysGlyTyrAspGlnProTyrVal 1260
 Db 3905 AGCGACAAAGATATGTTTATGATTCAGAAAGACATGAAGATATGAGAGCGGTATGTT 3964
 Qy 1261 LeuLeuGlnAmaLysGlnSerleuPheTyrIleYsaMetValGlnGlnleuGlyLysAlaGlu 1280
 Db 3965 TTGCTGCAAAATTAAGAGAGCGCTATTTTACAGATGTGTCAACACTGGGCAAGCAGAA 4024
 Qy 1281 AlaAlaAlaLeuThrGlnThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
 Db 4025 GCCGCTGCCCTCAGTGAACGCAAAACAGGATATCTTCAAAAGAAATTAATCACATATT 4084
 Qy 1301 GlyHisThrAspHisMetValThrAsnThrSerAenglyGlnProSerThrleuThrIle 1320
 Db 4085 GGTCACTGTGACCAATGTGTTTAAACAACCTTCAATGAGACAGCCCTCAACCTTAACTATT 4144
 Qy 1321 PheGlnThrAlaLeu 1325
 Db 4145 TTCCAGACAGCACTG 4159

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2006, 07:38:05 ; Search time 1691 Seconds
(without alignments)
5222.187 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6787
Sequence: 1 MLPVYQEKRPPLDANLCS.....MTWTSNGPSTLTFETAL 1325

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 496997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-O=/abs/ABSSWB_EPOC/US09976858/runat_13032006_170057_11733/app_query.fasta.1
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biocum62 -TRANS=humana.cdi -LIST=45
-DOCLALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=PCO -NORM=EXT -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=ABR08
-USER=US09976858 @CGN_1_1_727 @runat_13032006_170057_11733 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21.*

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2: geneseqn1908s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6787	100.0	3978	6	ABK92135
2	6787	100.0	3978	11	ADN39251
3	6785	99.9	5271	12	ADH10611
4	6785	99.9	5284	12	ADH10612

5	6785	99.9	5833	12	ADH10624	Adh10624 Human can
6	6785	99.9	5862	12	ADH10626	Adh10626 Human can
7	6781	99.9	4078	14	ADM14765	Adm14765 Tumour-ass
8	6779	99.9	4231	2	AAZ30078	AAZ30078 cDNA enco
9	6779	99.9	4231	5	AAH81778	AAH81778 Human dif
10	6779	99.9	4231	8	ABV75072	ABV75072 Human Dev
11	6779	99.9	4231	11	ADN39253	Adn39253 Cancer/an
12	6779	99.9	4231	14	ACL38944	Adl38944 ABCC4 cod
13	6779	99.9	4231	14	AEA00097	Aea00097 Human TAT
14	6779	99.9	4231	14	AEA00617	Aea00617 Human TAT
15	6779	99.9	4231	13	ADR66822	Adr66822 Human pro
16	6779	99.9	5832	13	ADR65919	Adr65919 Human pro
17	6779	99.9	5870	10	ADB75177	Adb75177 Prostate
18	6779	99.9	5871	14	ADX98506	Adx98506 Human ATP
19	6779	99.9	5871	14	ADZ49388	Adz49388 Insulin B
20	6779	99.7	4515	5	ABV24188	ABV24188 Human pro
21	6779	99.7	4515	5	ABV26511	ABV26511 Human pro
22	6779	99.7	4515	5	ABV20669	ABV20669 Human pro
23	6779	99.7	4515	5	ABV22410	ABV22410 Human pro
24	6779	99.7	4515	5	ABV24580	ABV24580 Human pro
25	6779	99.7	4515	5	ABV28224	ABV28224 Human pro
26	6760	99.6	6082	4	AAH93828	AAH93828 Human pro
27	6760	99.6	6082	4	AAH85142	AAH85142 Human pro
28	6760	99.6	6082	4	AAH85142	AAH85142 Human pro
29	6760	99.6	6082	5	ACA59729	ACA59729 Prostate
30	6760	99.6	6082	6	ABL95292	Abi95292 Human P51
31	6760	99.6	6082	8	ACC95456	Acc95456 Prostate
32	6760	99.6	6082	10	ADB13985	Adb13985 Human pro
33	6760	99.6	6082	10	ADG26401	Adg26401 Human can
34	6647	97.9	3913	12	ADQ59423	Adq59423 Human can
35	6600.5	97.3	6140	4	AAH93829	AAH93829 Human pro
36	6600.5	97.3	6140	4	AAH85143	AAH85143 Human pro
37	6600.5	97.3	6140	4	AAH85143	AAH85143 Human pro
38	6600.5	97.3	6140	5	ACAS9730	Acas9730 Prostate
39	6600.5	97.3	6140	6	ABL95293	Abi95293 Human P51
40	6600.5	97.3	6140	8	ACC95457	Acc95457 Prostate
41	6600.5	97.3	6140	10	ADB13986	Adb13986 Human pro
42	6600.5	97.3	6140	10	ADG26402	Adg26402 Human pro
43	6357	93.7	4395	10	ACC95747	Acc95747 Prostate
44	6357	93.7	4395	10	ADB14457	Adb14457 Expressio
45	6357	93.7	4395	10	ADG26980	Adg26980 Human pro

ALIGNMENTS

RESULT 1
ABK92135
ID ABK92135 standard; DNA; 3978 BP.
AC ABK92135;
DT 15-AUG-2002 (first entry)
DE Prostate cancer-associated DNA sequence #21.
KM Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX Mammalia.
XX OS
XX PN WO200230268-A2.
XX PD 18-APR-2002.
XX PF 12-OCT-2001; 2001WO-US032045.
XX PR 13-OCT-2000; 2000US-00687576.
XX PR 08-DEC-2000; 2000US-00733288.
XX PR 08-DEC-2000; 2000US-00733742.
XX PR 24-JAN-2001; 2001US-0263957P.
XX PR 16-MAR-2001; 2001US-0276791P.
XX PR 16-MAR-2001; 2001US-0276888P.
XX PR 06-APR-2001; 2001US-0281922P.

PR 24-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0288589P.
 XX
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX
 DR WPI; 2002-471335/50.
 DR P-PSDB; ABG61820.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 22; Page 316; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridize to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences
 CC
 XX
 SQ Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 3978
 Score: 6787.00 Matches: 1325
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 6 Gaps: 0
 US-09-976-858-42 (1-1325) x ABK92135 (1-3978)
 QY 1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
 DB 1 ATGCTGCCCGTGTACAGAGAGGTGAAGCCCAACCCGCTGCAGACCGCAACCTTGCTCA 60
 QY 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
 DB 61 CCGCGTCTTCTTGGTGGCTCAATCCCTGTTTAAATTGGCCATTAACGGAGATTAGAG 120
 QY 41 GluAspAspMetLysSerValLeuProGluAspArgSerGlnHisLeuGlyGlnLeu 60
 DB 121 GAAGATGATATGATATTCAGTGTGCAGAAACCGCTGCACAGACCTTGAGAGGAGTTG 180
 QY 61 GlnGlyPheTyrAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
 DB 181 CAAGGCTTCTGGATTAAGAAAGTTTMAAGCTGAGAAATGACGCACAGAAAGCTTCTTTA 240
 QY 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
 DB 241 ACAAGACATCATTAAGGTTTACTGAAATCTTATTTAGTTTGGAAATTTTACGTTA 300
 QY 101 IleGlnLysSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
 DB 301 ATTAGAAGAAAGTCCAAAGTAATCCAGCCCATATTTTGGAAATAATTATTAATTTT 360
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140

DB 361 GAAATTAATGATCCCATGATTTCTGTGCTTTGAACACAGGCTACGCTATGCCAGGTG 420
 QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
 DB 421 CTGACTTTTTCACGCTCATTTTGGCTTACTGATGATCACTATATTTTATTCACGTTGAG 480
 QY 161 CysAlaGlyMetCArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
 DB 481 TGTGCTGGAGTAGAGTTACGAGTAGCCATGTGCCATATGATTTATTCGAAAGCACTTGT 540
 QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
 DB 541 CTTACTATCATGCGCATATGGGAAAGACACACAGCCGATGATCACTGCTGTCAT 600
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTyrAlaGlyProLeu 220
 DB 601 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCTGTGGCAGACCACTG 660
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTyrMetGlnIleGlyIleSerCysLeuAlaGly 240
 DB 661 CAGGCGATCGCAGTACTGCTTCTGATGTGAGATGAGAAATATCGTGCCTTGCGG 720
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
 DB 721 ATGGCAGTTCTAATATCTCTCTGCTTGCAGAACTTTTGGAGATTGTTCTCATCA 780
 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 DB 781 CTGAGGAGTAAACATCGCAACTTTCACGATCCAGATCAAGAACATGAATGAATGATTA 840
 QY 281 ThrGlyIleArgIleIleLysMetLysAlaTrpGluLysSerPheSerAsnLeuIleThr 300
 DB 841 ACTGTTATTAAGAGTATTAATAATGACCCCTGGGAAAGTATTTTCAATCTTAATTAAC 900
 QY 301 AsnLeuArgLysLysGlnIleSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320
 DB 901 AATTGGAAGAAAGAGAAATTTCCAAAGTTCTGAGAGATTCTGCTCAGGAGGATGAT 960
 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
 DB 961 TTGGCTTGTGTTTTCAGTGAAGCAAAATCATCGTGTGAGACCTTCACCACTTACGTCG 1020
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
 DB 1021 CTCTCGGACAGTGTATCACAGCCAGCCGCTGTGCGAGTACGCTGTATGTGGGCT 1080
 QY 361 ValArgLeuThrValThrPhePheProSerAlaIleGluArgValSerGlnAlaIle 380
 DB 1081 GTGCGGCTGACGCTTACCTCTTCTTCCCTCAGCATTTGAGAGGTTGTCAGAGCATTC 1140
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGlnIleSerGlnArgAsnArg 400
 DB 1141 GTACAGCATCCGAAGATCAAGACCTTTTGTACTTATGAGATATTCACAGGCAACCGT 1200
 QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheThrAsp 420
 DB 1201 CAGTCCCGTCAGATGATGAAGATGTGTGATGTCAGGATTTTATCGCTTTTGGGAT 1260
 QY 421 LysAlaSerGlnThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyValLeu 440
 DB 1261 AAGGCATCAGAGACCCCAACTCTTACAGAGCTTCTTCTTACTGTACGCTGGCAATTG 1320
 QY 441 LeuAlaValAlaGlyProValGlyValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
 DB 1321 TTAGCTGTGTGTGCGCCGCTGGAGACAGGAAGTATCATCGTTAAAGTCCGTCTCGG 1380
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyValGlnIleAlaTyrValSerGln 480
 DB 1381 GAATTGGCCCCCAAGTCAAGGCGTGTGACGCGTCAAGAAAGATTCCTATGTGCTCAG 1440
 QY 481 GlnProTyrValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500
 DB 1441 CAGCCCTGGTGTCTCGGAACTCTGAGAGATTAATTTTATTTGGAGAAATATCAGA 1500

OY	501	LYSGIWAAGTYRGIULYSVALILEYVALACYSALALEUPLYSAAPLEUGINLEULEU	520
Db	1501	AAGGAACAGTATGAAAAAGTCATAAAGGCTGTGTCTGAAAAAAGATTTCACGTGTGG	1560
OY	521	GIUAAPGIIYAAPLEUTHVALILEGIYASAPARGIYTHTRHLEUSERGIYGIYGLNYS	540
Db	1561	GAGCATGTGATCTGCATCTGATAGAGATCCGGGACACACGCTGACGTGAGGGCAGAA	1620
OY	541	ALAARGVALAENLEUALARGALAVALTYPGLNAPALAAAPLIERYRLEULEUASAP	560
Db	1621	GCACGGGTAAACCTTGCAAGAGCAGCTGATCAAGATGCTGCATCTACTCTCGGACCAT	1680
OY	561	PROLEUSERALAVASAPALAGIULVALSERPRHISLEUPHEGLULEUCYBIIIECYGLN	580
Db	1681	CCTTCAGTGCAGTATGATCGGAACTTGACACACCTTGTCGAACTGTGATTTGTCA	1740
OY	581	ILEUHIAGIULYSEIETHRILEUVALTHRHISGLEUGINTYRLEULYSAALAA	600
Db	1741	ATTTTGCATGAGAAATACCAATTTTAGTACTCATCTAGTTGACGTACCTCAAGCTCA	1800
OY	601	SERGINILEUJILEULYASAPGIYLYSWECTVALGINULGELYTHTRYTRTHGIUPHE	620
Db	1801	AGTCAGATTCTGATTTTGAATGATTAATGGTGCAAGAGGGACTTACACGTGATTC	1860
OY	621	LEULYSERGIYILEASPHEGIYSERLEULEULYSLYASAPANGIULIUSERGIULIN	640
Db	1861	CTAAATATCTGATATGATTTTGCGCTCCCTTTTAAAGAAAGATATAGAGAAAGTCACA	1920
OY	641	PROPROVALPROGIYTHPROTHREULARGANARGTHRPHESERGIUSERSERVALTP	660
Db	1921	CCTCAGATCCGAGAACTCCCACTAAGAACTGACTTCCTCAGAGTCTTCGGTTTGG	1980
OY	661	SERGINIUSERSERIARPROSERLEULYASAPGIYALALEUGIUSERGIASAPHRGIU	680
Db	1981	TCTCAACATCTCTAGAACCCCTCTTGAAAGATGATGCTCTGGAAGCCAGATATCAAG	2040
OY	681	ASNVALPROVALTHREUSERGIULIUNASARGSERGIULYLYSVALGIPHEGLNLA	700
Db	2041	AATGCCCCAGTTACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTCAAGCC	2100
OY	701	TYRILYASERTYRPHARGIAGIYLAHISTPILIEVALPHEILEPHELEULILEULEU	720
Db	2101	TATAAGAAATTACTTCAGAGCTGTGTCTCACTGAGATTGCTTCATTTTCTTAATCTCTCA	2160
OY	721	ASANTHRAALAGIUNVALATYRVALLEUGINAPRTPLUSERTRYTRPALAASN	740
Db	2161	AACACTGCAGCTCAGGTGCCATATGTGCTTCMAAGTTGGTGGCTTCACTACGGGCAAC	2220
OY	741	LYSGIUSERMELEUASNVALTHRVALANGIYGIYASNVALTHRGIULYSLEUASP	760
Db	2221	AAACAAAGTATCTTAATATGCTCACTGTAATGAGAGGAAATGTAAACGAGAAAGCTAAT	2280
OY	761	LEUASNTPIYRLEUGIYILEYTSERGIYLEUTHRVALATHVALLEUPHEGLIYLE	780
Db	2281	CTTAACGTGACTTGAAGAAATTATTCAGGTTTAACGTGACCTACCGTTCTTTTGGCAT	2340
OY	781	ALAARGSERLEULEUVALPHEIYRVALLEUVALAENSERSEGINTHREUHIASNLYS	800
Db	2341	GCAACATCTCTATGTGATCTTCAAGCTCTGTGTTACTTTCACAAACTTTCGACAAACA	2400
OY	801	MECPHEGLUSERIILEULYSAIAPROVALLEUPHEPHEASAPASPROIIEGIYARG	820
Db	2401	ATGTTTGAAGTCAATTCGAAACCTCCGGATTAATCTTTGAATGAATCCAAATAGAAAG	2460
OY	821	ILELEUASARGPHESEIYASPIIEGIYHISLEUASAPLEULEUPROLEUTHRPH	840
Db	2461	ATTTTAATCGTTTCTCCAAABACATTGGACACTTGAGATTTCTGCGCTGCACGTTT	2520
OY	841	LEUASAPHEIIEGINTHREULEUGINVALIGIYVALVALSERVALALAVALAAVAL	860
Db	2521	TTAGATTTTCATCCAAACATTTGCTACAAAGTGTGTGTGTGTCTGTGTGCTGTGCGGTG	2580

QY	861	ILLEPRTPILEAIIETPROLEVALPROLEUGLYILELPEHELLEPHELEAARGX	880
DB	2581	ATTCCTTGAGATCGGAATACCTTGCTGCCCTGGATCATTTTCATTTTCTTGCGCGA	2640
QY	881	TYRPHLEUGLUTRISERARGSPVALLYARGLEUGLUSERTHTRARGSERPROVAL	900
DB	2641	TATTTTGGANAGCTCAAGAGATGTAGAGCGCTGGAACTTACACTCGAGTCCAGTG	2700
QY	901	PHESEHISLEUSERSESRSELEUNGILYLEUTRPHRILEARGALATYLYSALAGLU	920
DB	2701	TTTTCCCACTGTGATCTTCTCTCCAGGGGCTGGACCATCCGGGCGATCAAAAGCAGAA	2760
QY	921	GLUARGCYSGINGILUPEUPHEASPAALHISGLINAPLEUHISSERGIUALATRPHLEU	940
DB	2761	GAGAGGTGTCAAGAACTGTGTGAAGCACACAGAGATTACATTCAGAGGCTGGTCTTG	2820
QY	941	PHLEUTHRHSERARGTRPHPEALVALARGLEUPSPALAIACYSAIAMEPHEVAL	960
DB	2821	TTTTTGACAAAGTCCCTGGTGTGGCGCTCGCTGGATGCATCTGGCCATGTTGTGTC	2880
QY	961	ILEILEVALAPHEGLYSERLEULEUALYSRTHLEUPSPALAGLYGINVALGLY	980
DB	2881	ATCATCGTGGCTTGGGGTCCCTGATCTGGCAAAACTCGCATGCGGGGAGTTGGT	2940
QY	981	LEUALALEUSERTYRALALEUTHLEUMERGUYMERPHEGLINTRYSVALARGLINSER	1000
DB	2941	TTGGCACTGTGCTTATGCGCTTCAACCTCATGGGAGTGTTCAGTGTGTGTTCCGACAAAGT	3000
QY	1001	ALAAGLIVALGLUANMEEMELLESERVALGLUARGYALLLEGUYRTHRASPHEUGLU	1020
DB	3001	GCTAAGATGGAAATAGATGATTCAGTGAAGAAAGGTCACTGAATACACAGACTTGAA	3060
QY	1021	LYSGIUALAPROTRPGILUTYGINLYARGPROPROBROALATRPPOHISGLUGLYVAL	1040
DB	3061	AAAGAGACACTTGGGAATATCAGAAAGCCCAACCAACGCTGGCCCATGAGAGAGTG	3120
QY	1041	ILEILEPHEAPPAENVALAENPHEMETYRSEPROGILYGLYPROLEUVALLEULYHIS	1060
DB	3121	ATAATCTTGTGACATGTGAACCTTCATGTACAGTCAAGTGGGCTCTGTATCTGAACAT	3180
QY	1061	LEUTHRALALEULIELYBSERGINULYBVALGLYILEVALGLYARGTHRGILYALGLY	1080
DB	3181	CTGACAGACACTTAATAATCAAGAAAGGTGGCAATTGTGGGAAAGACCGAGCTGGA	3240
QY	1081	LYSSERSELEULIESERALALEUPHARGLEUSERGIUPROGIUGLYLYSILETPILE	1100
DB	3241	AAAGATTCCTTCATCTCAACCCCTTTTGAATGTTCAGAACCCGAAAGSTAAATTTGCATT	3300
QY	1101	ASPLYSIILEUTHRTHRGULILEGLYLEUHIASPLEUARGLYLYSMESERILEILE	1120
DB	3301	GATAAGATCTTGAACAACGAAATTGGACCTTCACGATTTAAGAAAGAAATGTCAATCATTA	3360
QY	1121	PROGINGIUPROVALLEUPHEMTHGLYTHMECARGLYBASNLEUAPPROPHEAENGILU	1140
DB	3361	CCTCAGGAACCTGTTTGTGTTCACCTGGAACATATGAGAAAAACCTGAGATCCCTTTAAAGAG	3420
QY	1141	HISRTHRAPSGIULUETRPAASALALEUNGILYVALGINLEULYSGIUTHRILEGLU	1160
DB	3421	CACACGGATGGGAACCTGTGGAATGCTTACAAAGSTTCAACTTTAAGAAACCATTTGAA	3480
QY	1161	ASPLEUPROGIULYSMEASPTRTHGLULEUALAGLUSERGYSEAPENPHESEVALGLY	1180
DB	3481	GATCTCTCGGTAAATAGATGATACGAAATTGGCAAAATCAAGATCCAAATTTTAAAGTGGGA	3540
QY	1181	GLINARGGLNEULVALCYBLEUALARGALALILEULARGLYBANGINILILEULILEILE	1200
DB	3541	CAAGAGACAACTGGGTGCTTGGCCAGGGGCAATTTCCAGAAAAATTCAGAAATGATTAATT	3600
QY	1201	ASPGIUALATHRALAENVALASPPROARGTHRAPSGIULEULILEGINLYSYLSILEARG	1220
DB	3601	GATGAGAGGAGCGGAATGTGATTCAGAACCTGATAGTTAATACAAAATAAAATCCGG	3660
QY	1221	GLIUYSPHEALAHISCYRTHVALLEUTHRILEALAHISARGLEUENRTHRIELEASP	1240

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Db      3661 GAGAAATTTGGCCCGTGCACCGCTGCTAACCATTTGACACAGATTGACACCATTTATTTGAC 3720
Qy      1241 SerrapylisilemValleuspergilyargleuyltyrAspGluProtyrVal 1260
Db      3721 AGCGAAGATATATGTTTATTTACATTCAGGAACATCGAAGATATGATGACCGGATATGTT 3780
Qy      1261 LeuleuginsnlysgluserleupherlyltyrMetValGlnGlnleuGlyAlaGlu 1280
Db      3781 TTGCTGCAAAATTAAGAGAGCGCTATTTTACAGATGCTGCAACATGCGGCAAGCAGAGA 3840
Qy      1281 AAlaAlaAlaLeuThGluThrAlaAlaAlaValtyrPheValArgAsnTyrrProHisIle 1300
Db      3841 GCCGCTGCCCTCAGCAACAGCAAAACAGGTATCTTCAAAAGAAATTTATCCACATATT 3900
Qy      1301 GlyHsThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
Db      3901 GGTCACTGACCAACATGCTTTCACACACTTCACATGACACCGCTCCAGCTTAACTATT 3960
Qy      1321 PheGluThrAlaLeu 1325
Db      3961 TTCCAGACAGCACTG 3975

RESULT 2
ADN39251
ID      ADN39251 standard; cDNA; 3978 BP.
XX
AC      ADN39251;
XX
DT      17-JUN-2004 (first entry)
XX
DE      Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:569.
XX
KW      Human; differential expression; cancer; angiogenic disorder;
KW      fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW      inflammatory disease; autoimmune disease;
KW      retinal neovascularisation syndrome; scarring; uterine fibroid;
KW      detection; diagnosis; prognosis; drug screening; drug targeting;
KW      wound healing; contraception; cytostatic; cardiac; immunomodulatory;
KW      vulnery; gene therapy; vaccine; gene; ss.
XX
OS      Homo sapiens.
XX
PN      WO2003042661-A2.
XX
PD      22-MAY-2003.
XX
PF      13-NOV-2002; 2002WO-US036810.
XX
XX
PR      13-NOV-2001; 2001US-0350666P.
PR      21-NOV-2001; 2001US-0332464P.
PR      29-NOV-2001; 2001US-0334393P.
PR      03-DEC-2001; 2001US-0335394P.
PR      14-DEC-2001; 2001US-0340376P.
PR      08-JAN-2002; 2002US-0347211P.
PR      10-JAN-2002; 2002US-0347349P.
PR      08-FEB-2002; 2002US-0355250P.
PR      13-FEB-2002; 2002US-0356714P.
PR      20-FEB-2002; 2002US-0359077P.
PR      29-MAR-2002; 2002US-0368809P.
PR      04-APR-2002; 2002US-0370110P.
PR      12-APR-2002; 2002US-0372246P.
PR      05-JUN-2002; 2002US-0386614P.
PR      16-JUL-2002; 2002US-0396839P.
PR      22-JUL-2002; 2002US-0397755P.
PR      22-JUL-2002; 2002US-0397845P.
PR      09-SEP-2002; 2002US-0409450P.
XX
XX
PA      (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI      Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Heverzi PA;
XX      Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
XX

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DR      WPI: 2003-468649/44.
DR      P-PSDB; ADN39252.
XX
PT      Determining the presence or absence of a pathological cell in a patient,
PT      useful for diagnosing, prognosing or treating cancer, comprises detecting
PT      a nucleic acid in a biological sample.
XX
PS      Claim 8; SEQ ID NO 569; 1385bp; English.
XX
CC      The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC      whose expression is upregulated or downregulated in specific cancers or
CC      other diseases such as angiogenic or fibrotic disorders, and to methods
CC      of determining the presence or absence of a pathological cell in a
CC      patient by detecting a nucleic acid at least 80% identical to those of
CC      the invention or by detecting a polypeptide of the invention. The
CC      invention also relates to expression vectors and host cells comprising a
CC      nucleic acid of the invention; antibodies which specifically bind a
CC      polypeptide of the invention; use of such antibodies for drug targeting;
CC      and methods of screening for modulators of activity or expression of the
CC      polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC      antibodies and methods are useful for diagnosing, prognosing and treating
CC      cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC      atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC      neovascularisation syndromes, scarring and uterine fibroids. They may
CC      also be useful in wound healing and in contraception. The present
CC      sequence represents a nucleic acid sequence of the invention.
XX
SQ      Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 3978
Score: 6787.00 Matches: 1325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0
XX
US-09-976-858-42 (1-1325) x ADN39251 (1-3978)
Qy      1 MetLeuPProValTYrGlnGluValIlyAspAsnProLeuGlnAspAlaAsnLeuCySer 20
Db      1 ATGCTGCCCGCTGACAGAGAGTGAAGCCCAACCGCTGCAAGACGCAACCTGCTGCA 60
Qy      21 ArgValPhePheTTPLeuAsnProLeuPheIlyIleGlyHsValArgArgLeuGlu 40
Db      61 CGCGGTTCCTTGCTGCTCAATCCCTGTTAAATGGCCATTAACGAGATTAGAG 120
Qy      41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisIleGlyGlnLeu 60
Db      121 GAAGATGATATGATTCAGTCTGCCAGAAAGCCGCTCAAGACCTTGAGAGAGATTG 180
Qy      61 GlnGlyPheTTPAsPlyGluValIleuArgAlaGluAsnAspAlaGlnIlyPProSerLeu 80
Db      181 CAGGGTCTCGGATTAAGAAAGTTTAAAGACTGAGATGACGACAGCAAGGCTTCTTA 240
Qy      81 ThrArgAlaIleIleIlyCySerTyrTyrPlySerTyrLeuValLeuGlyIlePheThrIleu 100
Db      241 ACAAGACCATCATTAAGTTACTGGAATCTTATTTAGTTGGGAATTTTTCATGCTTA 300
Qy      101 IleGluGluSerAlaIlyValIleGlnProIlePheIleGlyIlyIleIleAsnTyrrPhe 120
Db      301 ATTGAGAAAGTCCAAAGTATCCAGCCCAATTTTGGGAAAATTAATTATATTTT 360
Qy      121 GluAsnTyrAspProMetCAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140
Db      361 GAAATTTATGATCCATGATTTCTGTGCTTGAACACAGCTACGCTTACCGCAGGTG 420
Qy      141 LeuThrPheCyThrLeuIleLeuAlaIleLeuHisIleIlyTyrrPheTyrrHisValGln 160
Db      421 CTGACTTTTGGACGCTCATTTTGGCTATGCTATGCACTATTAATTTTATCACTGTAG 480
Qy      161 CysAlaGlyMetArgLeuArgValAlaMetCyHisMetIleTyrrArgValAlaLeuArg 180

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Db 481 TGTGCTGGGATGAGTTACGAGTACCATGTGCTCATATGATTTATCGAAGGACACTGCT 540
 Qy 181 LeuSerAsnMetAlaMetGlySerThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
 Db 541 CTTAGTAATGATGGCAATGGGAAAGACACACAGGCGCATATGATCATCTGTGCTGCAT 600
 Qy 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProLeu 220
 Db 601 GATGTGAACAAAGTTGATTCAGGTGACAGGTCTTACACTTCTGTGGGACAGACACTG 660
 Qy 221 GlnAlaIleValThrAlaLeuLeuThrMetGlyIleGlyIleSerCysLeuAlaGly 240
 Db 661 CAGGGGATCGCAGTACCTGCTACTGATGAGATGAGATTCGGAATTCGGCTCTGCGG 720
 Qy 241 MetAlaValIleuIleGileuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
 Db 721 ATGGAGATTCTAATCATCTCTGCTGCTGCAAGCTGTTTGGGAAGTGTTCATCA 780
 Qy 261 LeuAspSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 Db 781 CTGAGAGATGAACCTGCACACTTTCACGATGCCAGATCAGACCATGAAATGAATTA 840
 Qy 281 ThrGlyIleArgIleIleLysMetLysAlaArgIleLysSerPheSerAsnLeuIleThr 300
 Db 841 ACTGCTATTAAGATATATAAAATGATACGCTGGAAAGTCAATTTCAAACTTATTAAC 900
 Qy 301 AsnLeuArgLysLysGlyIleSerLysIleLeuAspSerSerCysLeuArgLysMetAsn 320
 Db 901 AATTGAGAAAGAAAGAGATTTCCAAAGATTCGAAGAGTTCTGCTCCACGGGGAGTAT 960
 Qy 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrVal 340
 Db 961 TTGGCTTCTGTTTTCAGTGCAGACCAAAATCATCGTTTGTGACCTTCAACCACTACG 1020
 Qy 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuThrValAla 360
 Db 1021 CTCCCTCGGAGTGTATCACACGCGCGTGTGCTGCGAGTACGCTGATGCGGCT 1080
 Qy 361 ValAlaGlyLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
 Db 1081 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCATTTGAGAGGGGTGCACAGCAATC 1140
 Qy 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGlyIleSerGlnArgAsnArg 400
 Db 1141 GTACAGATCCGAAAGATCCAGACCTTTTGTGCTACTGATGAGATTCACAGGCGCAACCT 1200
 Qy 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheThrAsp 420
 Db 1201 CAGCTGCCGTGATGTGTAAAGATGGTGCATGTGCAGATTTTACTGCTTTTGGGAT 1260
 Qy 421 LysAlaSerGlyThrProThrIleuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
 Db 1261 AAGGATCATGAAACCCCAACTCTACAGGCTTTCTTCACTGTACAGCTGCGCAATTCG 1320
 Qy 441 LeuAlaValAlaGlyProValGlyValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
 Db 1321 TTAGCTGTGTGTGCGCCCTGCGGAGCAGGAAAGTCACTCTTAAAGTCCGCTGTCGCG 1380
 Qy 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaIleValSerGln 480
 Db 1381 GAATTGCGCCCAAGTCAAGGCTGTGTGAGCTGTGCATGGAAGAATTCGCTATGTCTCAG 1440
 Qy 481 GlnProThrPheValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysArgIle 500
 Db 1441 CAGCCCTGGTGTCTCGGAACTCGAGAGTAAATATTATTATTTGGGAAGAAATACAA 1500
 Qy 501 LysGluArgLysArgLysValIleLysValCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 Db 1501 AAGGAACATATGAAAAAGTCTAAAGGCTTGTGCTGAAAAAGAAATTTACAGCTGTTCG 1560
 Qy 521 GlnAspGlyAspLeuThrValIleGlyAspArgLysThrThrLeuSerGlyGlyGlnLys 540
 Db 1561 GAGGATGTGTGATCTGACTGTGATGAGATCGGGAAACACGCTGATGTGAGAGGACGAAA 1620

Qy 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
 Db 1621 GCAGGGATTAACCTTTCAGAGCAAGTGTATCAAGATCTGTGACATCTATCTCTGACAT 1680
 Qy 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
 Db 1681 CCTTCAGTGCAGTAAAGATGGGAAAGTTAGCAGACCTTGTTCGAACTGTGATTTGTCAA 1740
 Qy 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnThrThrLeuValAla 600
 Db 1741 ATTTTCATGGAAGATTCACAAATTTAGTGTCACTACCTGTTCAGATTCCTCAAGCTGCA 1800
 Qy 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
 Db 1801 AGTCAGATTCTGATATTGAAGATGTGAATGTGTGCAAGAGGGACTTACCTGAGTTC 1860
 Qy 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluLeuSerGluGln 640
 Db 1861 CTAAATATGCTATTAAGATTTTGGCTCTTTAAAGAAAGATTAATGAGAAAGTGAACA 1920
 Qy 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlySerSerValTyr 660
 Db 1921 CCTCCAGTTCAGGAACTCCCACTAAGGAAATGTACCTTCTCAGAGTCTTGGTTCG 1980
 Qy 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGlu 680
 Db 1981 TCTCAACATTTCTTACGCTCTCTGTAAGATGTGTCTGAGAGCCCAAGATACAGAG 2040
 Qy 681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
 Db 2041 AATGTCCAGTATCATATCATCAGAGAGAACCGTTCTGAAGAAAGTTTGTTTCAGGCC 2100
 Qy 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTyrIleValPheIlePheLeuIleLeuLeu 720
 Db 2101 TATTAAGATTTACTCAGAGCTGTGTCTCACGGAATTCCTTCAATTTCTTATCTCTCTA 2160
 Qy 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrProThrLeuSerTyrThrAlaAsn 740
 Db 2161 AACACTGAGCTCAGGTGTGCTTATGTCTTAAAGATGTGTGCTTCACTACCTGCGCAAC 2220
 Qy 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyAsnValThrGluLysLeuAsp 760
 Db 2221 AAACAAAGTATGCTAAATGTACCTGTAATGAGAGGAATGTAAACGGAAGCTGAT 2280
 Qy 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
 Db 2281 CTTAACCTGTACTTGAAGATTTATTCAGTTTAACTGTACCTCCGTTCTTTTGGCATA 2340
 Qy 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
 Db 2341 GCAGATCTCTAATGTGTATTCGCTGTGTAACTCTTCAAACTTTCACAACTTGCACAA 2400
 Qy 801 MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
 Db 2401 ATGTTTGAATGATTCGAAAGCTCCGCTATATCTTTGATTAAGATTCGAATGGAAGA 2460
 Qy 821 IleLeuAsnArgPheSerLysAspIleGlyHisIleLeuAspAspLeuLeuProLeuThrPhe 840
 Db 2461 ATTTTAAATCGTTTCTCCAAAGACATTCGACACTTGTGATTTGCTGCGCTCAGCTTT 2520
 Qy 841 LeuAspPheIleGlnThrLeuGlnValValGlyValValLysSerValAlaValAlaVal 860
 Db 2521 TTAAATTCATCCAGACATTTGCTACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
 Qy 861 IleProThrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
 Db 2581 ATTCCTTGATCGCAATACCTTGTTCCTTGTGATTCATTTTCTTCTGCGGA 2640
 Qy 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900
 Db 2641 TATTTTGGAAACGTCAAGAGATGTGAAGGCTCGGAATCTCACTACGAGATCGCAGTG 2700

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QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
DB 2701 TTTTCCCATCTTGTCACTTCTCTCCAGGGGCTCTGGACATCCGGGCATCAAGACAGA 2760
QY 921 GluArgGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
DB 2761 GAGAGGTGTCAGAACTGTTTATGACACACAGATTTCATTCAGAGCTTGTTCTTG 2820
QY 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
DB 2821 TTTTGGACACGTCCTCCGCTGCTCCGCTCCGCTGATGATCCATCTGTCCATGTTTGT 2880
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
DB 2881 ATCATGCTGGTCCCTTGGGCTCCCTGATTCGGCAAAACTCTGGATGCCGGACAGTTGCT 2940
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
DB 2941 TTGGCAGCTGTCTATGCTCCCTCAGCTCAGTGGGAGATTTCAGTGTGTTGACAAAGT 3000
QY 1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
DB 3001 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGATCATTAATACACAGCTTGA 3060
QY 1021 LysGluAlaProTrpGluTyrGlnLysArgProProAlaTrpProHisGluGlyVal 1040
DB 3061 AAAGAAGCACCCTGGGATATATCAAGAAACCCACACCTGGGCCCATGAAGAGAGT 3120
QY 1041 IleIlePheAspAsnValAsnMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
DB 3121 ATAACTTTTGACAAATGTAATTCATGTAAGTCCAGTGGGCTCTGTGACTGAAGCAT 3180
QY 1061 LeuThrAlaLeuIleLysSerGlnGlyLysValGlyIleValGlyArgThrGlyAlaGly 1080
DB 3181 CTGACGACCTCATTAATCAACAGAAAGCTTGGATCTTGGAAAGAACCGGAGCTGA 3240
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
DB 3241 AAAAGTTCCTCATCTCAGCCCTTTTATGATTGTGAGAAACCCGAAAGTAAATTTGGATT 3300
QY 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysMetSerIleIle 1120
DB 3301 GATTAAGATTTGACAACTGAATTTGACATTCAGATTTAAGAAAGAAATGTCAAATCATA 3360
QY 1121 ProGlnGluProValLeuPheThrGlyTyrMetArgLysAsnLeuAspProPheAsnGlu 1140
DB 3361 CCTCAGGAACCTGTTTGTCTTCACTGCAACATGAGAAAGAAACCTGATCCCTTATATG 3420
QY 1141 HisThrAspGluGlnLeuThrPheAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
DB 3421 CACACGATGAGGAAGTGTGAATGCTTACAAAGAGTCAACTTAAGAAACCATTTGA 3480
QY 1161 AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGly 1180
DB 3481 GATCTTCCGTAATAATGATCTGAATTAAGCAATTCAGAAATTCATTTAGTGTGGA 3540
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
DB 3541 CAAGGCAACTGCTGTGCTTCCAGGCAATTCAGAGAAATCAAGATATGATTTAT 3600
QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
DB 3601 GATGAAGCAGCGCAATGATGATCCAGAACTGATGATTAATCAAAAAAATCCCG 3660
QY 1221 GluLysPheAlaHisGlyThrValLeuThrIleAlaHisArgLeuSerThrIleIleAsp 1240
DB 3661 GAGAAATTTTGGCCACGACCGTGTACCATTTGCAACAGATTTGAACCATTAATTTGAC 3720
QY 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
DB 3721 AGGGAACAAGTAAATGTTTATGATTCAGAGAGCATGAAGAAATATATATGACCGTATGTT 3780
QY 1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280

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DB 3781 TTTGTCGCAAAATTAAGAGGCTATTATTACAAAGATGGTGCAACACTGGGCAAGCAANA 3840
QY 1281 AlaAlaAlaLeuThrGlnThrAlaLysGlnValTyrPheLysAsnTyrProHisIle 1300
DB 3841 GCCGCTGCCCTCAGTGAACAGCAAAACAGGTAATCTTCAGAAAGAAATTAATCACTATT 3900
QY 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
DB 3901 GGTCACTGACCAATGATGTTTACAAACACTTCATATGACAGCCCTGACCTTAATTAAT 3960
QY 1321 PheGluThrAlaLeu 1325
DB 3961 TTCGAGACAGCACTG 3975
RESULT 3
ADH10611
ID ADH10611 standard; DNA; 5271 BP.
XX
AC ADH10611;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human cancer-related polynucleotide, SEQ ID 1.
XX
KW Cancer-related gene; prostate cancer; cytosolic; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003104404-A2.
XX
PD 18-DEC-2003.
XX
PF 05-JUN-2003; 2003WO-US017772.
XX
PR 06-JUN-2002; 2002US-0386651P.
XX
PA (AVAL-) AVALON PHARM INC.
XX
PI Ebner R.
XX
DR WPI; 2004-062332/06.
XX
PT Identifying agents that modulate the activity of cancer-related gene,
PT compound for treating or diagnosing prostate cancer comprising contacting a
PT compound with a cell containing a gene under conditions promoting
PT expression of the gene.
XX
PS Claim 1; SEQ ID NO 1; 79pp; English.
XX
CC The invention relates to identifying an agent that modulates the activity
CC of a cancer-related gene. The method involves contacting a compound with
CC a cell containing a gene that corresponds to a polynucleotide having a
CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
CC expression of the gene. The method is useful for identifying an agent
CC that modulates the activity of a cancer-related gene. The polypeptides
CC and antibodies of the invention are useful for treating and diagnosing
CC cancer, preferably prostate cancer. It is also useful for screening
CC assays for agents that are effective in reducing the activity of cancer-
CC related genes. The present sequence represents a specific example of a
CC cancer-related polynucleotide sequence.
XX
SQ Sequence 5271 BP; 1480 A; 1087 C; 1212 G; 1492 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 5271
Score: 6785.00 Matches: 1324
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.9% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 12 Gaps: 0
US-09-976-858-42 (1-1325) x ADH10611 (1-5271)

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QY MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
 Db ATGCGCCCGGTTCACAGAGGTGAAGCCCAACCCGCTGCAGACCGCAACCTGCTCA 175
 QY ArgValPhePheTrpLeuAsnProLeuPheLysIleGlyHisLeuArgArgLeuGln 40
 Db CGCGGTTCCTTGGGGGTCAATCCCTGTTAAATGGCCATTAACCGAGATTAGG 235
 QY GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
 Db GAAGATGATATGTATTCAGTGTCCAGAGAGCCCTCAACGACCTTGGAGAGAGTTG 295
 QY GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
 Db CAAAGGTTCGGATTAAGAGAGTTTAAAGCTGAGAAAGACGACACAGAGCTTCTTTA 355
 QY ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
 Db ACAAGAGCAATCATTAAGTTTACTGGAAATCTTATTTAGTTTGGAAATTTTACGTTA 415
 QY IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleLeuAsnTyrPhe 120
 Db ATTGAGAAAGTGCACAAAGTATCCAGCCCATATTTTGGGAAATTAATTAATTTT 475
 QY GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
 Db GAAATTAATGATCCATGATTCGTGGCTTGAACACAGCGTACGCTACGCTACGCGGG 535
 QY LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
 Db CTGACTTTTGGACGCTCATTTTGGCTATACCTGATCACTTATATTTTATACCTTCAG 595
 QY CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
 Db TGTGTGGGATGAGGTTCAGAGTACCCATGTGCCATATGATTAATTCGAGAGGCACTTGT 655
 QY LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerLeu 200
 Db CTTAATTAACATGCGCATGGGAGAGAACACACAGGCGCATATGATCAATCTGTGTCAT 715
 QY AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
 Db GATGGAACAAGTTTGATCAGGTGACAGTCTTACACTTCTGTGGGAGGAGCACTG 775
 QY GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlyIleGlyIleSerCysLeuAlaGly 240
 Db CAGCGGATCGCAGTACCTGCTTCTGATGAGATAGAAATTCGTGCTGCTGGG 835
 QY MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
 Db ATGGCAGTTCTTAATCATCTCTGCTTGGCAAACTGTTTGGAGAGTGTCTTCATCA 895
 QY LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 Db CTGAGGAGTAAACCTGCAACTTTCACGATGCGACAGATCAGGACATGATTAATTA 955
 QY ThrGlyIleArgIleIleLysMetTyrAlaTrpGlyLysSerPheSerAsnLeuIleThr 300
 Db ACTGATATAGAGATATATTAATATGATGCTGGGAAAGTCAATTTCAATCTTATATAC 1015
 QY AsnLeuArgLysGlyLysGlyLysSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320
 Db AATTTGAAGAAAGAGAGATTTTCAAGATTTCTGAAGAGTTCTGTGCTCAAGGGAGAT 1075
 QY LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
 Db TTGGCTTGCTTTTCAAGCAAGCAAAATCATCGTGTGTCACCTTCAACCACTACGTC 1135
 QY LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
 Db CTCCTCGGACAGTGATCAGACGCGCGTGTGTGTCGACGTGATCACTGTATGGGCT 1195

QY ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGlnAlaIle 380
 Db GTGCGGTGAGCGTTTACCTTCTTCCCTCAACCATTAAGAGGTTCAGAGGCATTC 1255
 QY ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGlyIleSerGlnArgAsnArg 400
 Db GTCAAGCATCCGAAAGATCAGACCTTTTGGCTACTGTATGAGATTCACACGCAACCGT 1315
 QY GlnLeuProSerAspGlyLysLysMetValHisValGluAsnPheThrAlaPheTrpAsp 420
 Db CAGCTGCGGTAGATGTGAAGATGGTGTGATGTGACGAGATTTTACGCTTTTGGGAT 1375
 QY LysAlaSerGluTrpProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
 Db AAGGATCAGAGACCCCACTTCAAGGCTTCTTCTTACTGTCAAGCTGGGCAATTG 1435
 QY LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
 Db TTAGCTGTGTGCGGCCCGTGGAGCAGGAGATCATCATGTTAAGTCCGTGCTCGG 1495
 QY GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
 Db GAATTTGGCCCAAGTCAAGGCGTGTGCGTGTGATGAGAAATTTGCTATGTGTCTGAG 1555
 QY GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500
 Db CAGCCCTGGGTGTCTCGGAGACTCTGAGGCTATATTTTATTTGGAGAAATATTA 1615
 QY LysGluArgTyrGlyLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 Db AAGGACGATATGAAAAAGTCATTAAGGCTTGTGCTGAAAAAGATTTACAGTGTGG 1675
 QY GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
 Db GAGATGTGTATTCGACTGTATAGAGATGCGGAGAACACAGCTGAGTGGAGGCGAGAA 1735
 QY AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
 Db GACGGGTAAACCTTGCAGAGCAGTGTATCAAGTGTGCATCTATCTCTGAGCAT 1795
 QY ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
 Db CCTCTCAGTGCAGTATGATGCGGAAGTTAGCAGACCTTGTGCAACTGTGATTTGTCA 1855
 QY IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
 Db ATTTTGCATGAGAAATCATCAATTTTATGTGATCATCATGTCAGTACCTCAAGCTGCA 1915
 QY SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
 Db AGTCAGATTCGATATTAAGATGTAAATGGTGCAAGAGGGGACTTATCACTGAGTTC 1975
 QY LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGlnGln 640
 Db CTAAATCTGATATAGATTTTGGCTCTCTTTTAAAGAGATATAGAGAAAGTGAACA 2035
 QY ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
 Db CCTCCAGTTCAGAGAACTCCACACTAAGCAATGTATCTTCTCAAGTCTTCCGTTGG 2095
 QY SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGlu 680
 Db TCTCAACATCTTCAAGCTCTCTCTTGAAGATGTGTCTGAGAGCACAAGTACAGAG 2155
 QY AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
 Db AATGCCAGTTATCATCATCAGAGAGAACCGTTCTGAAGAGAAAGTTTGTTTCAGGCC 2215
 QY TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
 Db TATTAAGATTAATCTCAGAGCTGTGCTCAGCTGATTTCTTCAATTTCTTATATCTCTTA 2275
 QY AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpLeuSerTyrTrpAlaAsn 740

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|||||
Db AACACGACGACGACGAGTCCATATGCGCTTCAAGATGGTGGCTTCACTACGCGCAAC 2335
|||
QY LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGlnValSerLeuAsp 760
|||
Db AAACAAGATGCTAAATGCTCACTGAATGAGGAGGAAAGTAAACGAGAGCTGAGAT 2395
|||
QY LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
|||
Db CTTAACTGGTACTTGAAGATTTATTCAGGTTTAACTGATGACGCTCTTTTGGCATA 2455
|||
QY AlaAspSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
|||
Db GCAGATCTCTATTGGTATTCTACGCTCTGTTAACTCTTCAAACTTGCACAAACAA 2515
|||
QY MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspAspAspProIleGlyArg 820
|||
Db ATGTTTGAATCAATCTGAAAGCTCCGATTAATTTCTTGAATGAATCAATGAGAGAA 2575
|||
QY IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
|||
Db ATTTTAAATCGTTTCTCCAAAGACATGAGACCTTGAGATTTGCTGCGCGTGAAGTTT 2635
|||
QY LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
|||
Db TTAGAATTCATCCAGACATTTGCTACAAAGTGGTGGTGGTCTGCTGCTGGCGCCGTG 2695
|||
QY IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
|||
Db ATTCCTTGATCGCAATACCTTGTTGTTCCCTTGGAAATCAATTTCTTCTGGCGCA 2755
|||
QY TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900
|||
Db TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGAATCTTCAACTCGAGTCCAGTG 2815
|||
QY PheSerHisLeuSerSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
|||
Db TTTTCCACCTTGCATCTTCTCCAGGGGCTCTGACCATCCGGGCAATACAAAGAGAA 2875
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QY GlnArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeu 940
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|||
QY PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db TTTTGGACAAACGTCGCGTGGTTCGCGCGTCTGGATGCCATCTGTCCATGTTTGTG 2995
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QY IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
|||
Db ATCATCGTTGCGCTTGGGTCCCTGATTCGGCAAAACCTGGATGCCGGCAGGTTGCT 3055
|||
QY LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
|||
Db TTGGGACCTGCTCATGCGCTCACGCTCAGGGGATTTTCAGTGGTGTGCAAAAGT 3115
|||
QY AlaGlnValGlnAsnMetMetIleSerValGlnArgValIleGlyLysThrAspLeuGln 1020
|||
Db GCTGAAGTTGAGATATGATGATCTCAGTGAAGGAGTCAATTAACACAGACTTGA 3175
|||
QY LysGlnAlaProTrpGlyTyrGlnLysArgProProProAlaTrpProHisGlyVal 1040
|||
Db AAAGAGACACTTGGGATATCAGAAACGCCCAACCAAGCCGCGCCATGAGAGAGTG 3235
|||
QY IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
|||
Db ATTAATCTTGAACAATGTAATCTCATGTACAGTCCAGGGGCTCTGAGTACTGAAGCAT 3295
|||
QY LeuThrAlaLeuIleLysSerGlnGlnLysValGlyIleValGlyArgThrGlyAlaGly 1080
|||
Db CTGACAGCACTCATTTAAATCAACAAGAAAGTTGGGATTTGGGAGAAACCGGAGCTGA 3355
|||
QY LysSerSerLeuIleSerAlaLeuPheArgLeuSerGlnProGlnGlyLysIleTrpIle 1100
|||

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Db 3356 AAAAGTCCCTCATCTCAGCCCTTTTAGATGTGCAGAACCCGAGGATGAAAAATTGCAAT 3415
|||
QY AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
|||
Db GATTAAGATCTTGACAACTGAAATTTGACTTACAGATTTTAAAGAAAGAAATGCAATCAT 3475
|||
QY ProGlnLysProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
|||
Db CCTCAGAAACCTGTTTGTTCATCTGGAACAAATGAGGAAAAAAGCTGGATCCCTTTAATGAG 3535
|||
QY HisThrAspGlnGlnLeuTrpAsnAlaLeuGlnGlnValGlnLeuLysGlnThrIleGln 1160
|||
Db CACAGAGATGAGGAACTGTGAATGCTTTTACAGAGGTACAACTTAAAGAAACCAATTGA 3595
|||
QY AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGly 1180
|||
Db GATCTTCTGTGTAATGATGATGATGATTTAGCAGATGAGATCCAAATTTAAGTGTGA 3655
|||
QY GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
|||
Db CAAAGACAACTGTGTGCTTGCCAGGCAATTCACAGAAAAATCAGATATTGATTATTT 3715
|||
QY AspGlnAlaThrAlaAsnValAspProArgTrpHisAspGlnLeuIleGlnLysLysIleArg 1220
|||
Db GATGAAGCGAGCGCAATGTGATCTCAAGAACTGATGATTAATCAAAAAAATTCGCG 3775
|||
QY GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
|||
Db GAGAAATTTGCCCACTGACCGTGTATCACTTGCACACAGATTAACCACTATTGAC 3835
|||
QY SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlyTyrAspGlnProTyrVal 1260
|||
Db AGCGAACAATGATGTTTATGATTCAGAAAGACTGAAAGAAATGAGAGCGTATGTT 3895
|||
QY LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGln 1280
|||
Db TTGCTGCAAAATAAAGAGGCTTATTTTACAAAGATGTGCACACATGGAGGACAGAA 3955
|||
QY 1281 AlaAlaAlaLeuThrGlnThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
|||
Db GCCGCTGCCCTCAGCAAGAAACAGAAACAGATATATCTCAAAAGAAATTAATCCATATTT 4015
|||
QY GlnHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
|||
Db GGTTCACACTGACCAATGTTTAAACAACTTCATATGACAGCCCTCCACCTTAATATTT 4075
|||
QY PheGlnThrAlaLeu 1325
|||
Db 4076 TTGAGACAGCACTG 4090
|||

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RESULT 4
 ADH10612
 ID ADH10612 standard; DNA; 5284 BP.
 XX ADH10612;
 AC 11-MAR-2004 (first entry)
 XX DT
 XX DE Human cancer-related polynucleotide, SEQ ID 2.
 XX KW Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.
 OS Homo sapiens.
 PN WO2003104404-A2.
 PD 18-DEC-2003.
 XX 05-JUN-2003; 2003WO-US017772.
 XX PF
 XX 06-JUN-2002; 2002US-0386651P.
 XX PR
 XX (AVAL-) AVALON PHARM INC.

XX Ebner R;
XX MPI: 2004-062332/06.
XX
XX Identifying agents that modulate the activity of cancer-related gene,
XX useful for creating or diagnosing prostate cancer comprising contacting a
XX compound with a cell containing a gene under conditions promoting
XX expression of the gene.

PS Claim 1; SEQ ID NO 2; 79pp; English.

XX The invention relates to identifying an agent that modulates the activity
XX of a cancer-related gene. The method involves contacting a compound with
XX a cell containing a gene that corresponds to a polynucleotide having a
XX sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
XX expression of the gene. The method is useful for identifying an agent
XX that modulates the activity of a cancer-related gene. The polypeptides
XX and antibodies of the invention are useful for treating and diagnosing
XX cancer, preferably prostate cancer. It is also useful for screening
XX assays for agents that are effective in reducing the activity of cancer-
XX related genes. The present sequence represents a specific example of a
XX cancer-related polynucleotide sequence.

Sequence 5284 BP; 1480 A; 1138 C; 1210 G; 1456 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 5284
Score: 6785.00 Matches: 1324
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.9% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 12 Gaps: 0

US-09-976-858-42 (1-1325) x ADH10612 (1-5284)

Qy 1 MetLeuProValIyGInGluValIyPProAenProLeuGInAAspAlaAsnLeuCySer 20
Db 116 ATGCGCCCGTGTACAGAGAGGTGAAGCCCAACCGCTGACAGAGCCCAACCTGCTCA 175
Qy 21 ArgValPhePheTyrTrpLeuAanProLeuPheUyIleGInIleUyAArgArgLeuGIn 40
Db 176 CGCGGTTCTTCTGGTGGCTCAATCCCTGTTAAATGGCCATTAACGAGATTAGAG 235
Qy 41 GluAAspAerMetYySerValLeuProGInAAspAerGInIleUyGInLeu 60
Db 236 GAAAGTGAATGATGATTCAGTGTGTCAGAAAGCCGCTCACAGCACTTGGAGAGAGTTG 295
Qy 61 GInGlyPheTyrAAspLyGInValIleuAArgAlaGInAAspAlaGInIySerProSerLeu 80
Db 296 CAAAGGTTCTGGAGTAAAGAAAGTTTAAAGCTGAGATGAGCGCACAGAAAGCTTCTTTA 355
Qy 81 ThrAlaIleIleIleUyCyATyTrpIySerTyIleUyValIleUyIlePheThrLeu 100
Db 356 ACAAGAGCAATCATTAAGTGTACTGAAATCTTATTAGTTTGGAAATTTTACGTTA 415
Qy 101 IleGInUySerAlaIyValIleGInProIlePheUyGInIleUyIleAsnTyIle 120
Db 416 ATTGAGAAAGTGCACAAAGTATTCAGCCCAATTTTGGGAAATTAATTAATTAATTT 475
Qy 121 GluAenTyAAspProMetAAspSerValAlaLeuAenThrAlaTyAlaTyAlaThrVal 140
Db 476 GAAATTTATGATCCATGATTTCTGGCTTTGAACAGCGCTAGCGCTTAGCCAGGTG 535
Qy 141 LeuThrPheCyThrLeuIleUyAlaIleUyIleUyIleUyIleUyIleUyIleUyIle 160
Db 536 CTGACTTTTGGACGCTCATTTTGGCTATGCTGACCACTTATATTTTATACGTTGAG 595
Qy 161 CysAlaGlyMetAArgLeuAArgAlaAlaMetCysIleUyIleUyIleUyIleUyIleUy 180
Db 596 TGTGTGGAGTGAAGGTTCAGAGTACCATGTGCCATATGATTTTATCGAAGGCACTTGT 655
Qy 181 LeuSerAenMetAlaMetGlyUyThrThrThrGInIleValIleAsnLeuUySerAen 200

Db 656 CTTAGTAACTGGCCATGGGAGAGCAACACAGGCCAGATATGCAATCTGCTGCCAAT 715
Qy 201 AspValAenUyPheAAspGInValIleUyIleUyIleUyIleUyIleUyIleUyIleUy 220
Db 716 GATGTGAACAAAGTTTGAACAGGTGACAGTGTCTTACCTTCTGTTGGAGAGACACTG 775
Qy 221 GInAlaIleAlaValIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUy 240
Db 776 CAGCGATGCGAGTACCTGCTTACTGATGAGATGAGAAATTCCTGCTGCTGCTGCTG 835
Qy 241 MetAlaValIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUy 260
Db 836 ATGGAGTGTCAATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
Qy 261 LeuAAspSerTyThrAlaThrPheThrAAspAlaArgIleAArgIleAArgIleAArg 280
Db 896 CTGAGAGTAAACCTGCAACTTTCACCGATCCAGATCCAGAGACCATGAAAGTTATTA 955
Qy 281 ThrGlyIleAArgIleIleUyMetTyAlaIleUyIleUyIleUyIleUyIleUyIleUy 300
Db 956 ACTGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1015
Qy 301 AsnLeuAArgUyLyGInIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUy 320
Db 1016 AATTGAGAAAGAGAGATTTCAGAGTCTGAGAGTCTGCTGCTGCTGCTGCTGCTGCTG 1075
Qy 321 LeuAlaSerPhePheSerAlaSerUyIleIleValIlePheValIleUyIleUyIleUy 340
Db 1076 TTGGCTTCTGTTTTCAGTGCAAGCAAAATCATCGTGTGTGATGATGATGATGATGAT 1135
Qy 341 LeuUyGInSerValIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUyIleUy 360
Db 1136 CTCTGCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195
Qy 361 ValAArgLeuThrValIleUyPhePhePheProSerAlaIleGInAArgValSerGInUy 380
Db 1196 GTGGGCTGAGAGTATACCTCTTCTTCCCTCACACATGAGAGGTGTACAGAGCAATC 1255
Qy 381 ValSerIleAArgArgIleGInThrPheUyLeuUyAAspGInIleUyIleUyIleUy 400
Db 1256 GTGACATCCCAAAATCCAAACCTTTTGTCTTGTGATGATGATGATGATGATGATG 1315
Qy 401 GInUyProSerAAspGlyUyIleUyMetValIleUyIleUyIleUyIleUyIleUyIle 420
Db 1316 CAGCTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1375
Qy 421 LyAlaSerGInUyThrProThrLeuGInIyUySerPheThrValAArgProGlyUyLeu 440
Db 1376 AAGGATCAAGAGACCCCAACTCTCAAGGCTTCTTACTGTCAGACCTGGGGAATTG 1435
Qy 441 LeuAlaValIleGlyProValIleUyAlaGlyUySerSerLeuUySerAlaValIleUy 460
Db 1436 TTACCTGTGTGCGGCGGCTGGAGAGAGATCATCATCGTTAAAGTCCGCTGCGG 1495
Qy 461 GluUyAAspProSerIleGlyUyValSerAlaIleGlyAArgIleAlaTyValSerGIn 480
Db 1496 GAATTTGCCCCCAAGTCAAGGCTGTGTCAGCGTGAAGAAATTTGCTATGTGCTGAG 1555
Qy 481 GInProTyValIleUySerGlyIleUyAArgSerAenIleUyPheGlyUyIleUyTyGIn 500
Db 1556 CAGCCCTGGGTTCTGCGGAACTCTGAGAGATTAATTTTATTTGGAGAAATATGAA 1615
Qy 501 LyGInUyArgTyGInUyValIleUyAlaCysAlaLeuUyUyAAspLeuGInLeuUy 520
Db 1616 AAGCAACATATGAAAAAGTATTAAGCTTGTGCTGAAAAAGATTTTACACTGTG 1675
Qy 521 GluUyPheGlyAAspLeuThrValIleGlyAAspAArgGlyIleUyIleUyIleUyIle 540
Db 1676 GAGGATGTGTATGACTGTGATGAGATGAGGAGATGAGGAGATGAGGAGGAGGAGGAG 1735
Qy 541 AlaArgValAenLeuAlaArgAlaValIyGInAAspAlaAspIleTyIleUyLeuAAsp 560

Db 1736 GCACGGGTAAACCTTGCAAGACAGTGTATCAAGATGCTGACATCTATCTCCGACGAT 1795
 QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysGln 580
 Db 1796 CCTCTCAGTGCAGTATGATGCGGAAGTTAGCAACACTTGTGCAACTGTGTATTTGTCA 1855
 QY 581 IleLeuHisGluLeuValLeuThrIleLeuValThrHisGlnLeuGlnTyrIleuValAla 600
 Db 1856 ATTTTGCAATGAGAAAGATCACAATTTTAGTACATCACTGACAGTACTCAAGAGCTGCA 1915
 QY 601 SerGlnIleLeuIleLeuValSerArgIleValMetValGlnLeuGlyThrTyrThrGluPhe 620
 Db 1916 AGTCAGATTCTGATATGTGAAGAATGCTAAATGTGTCAAGAGGAGCTTACACTGATGTC 1975
 QY 621 LeuValSerGlyIleAspPheGlySerLeuLeuValValAspAsnGluGlnSerGlnGln 640
 Db 1976 CTAAATCTGTATATGATTTTGGCTCCCTTTTAAAGAGATTAATGAGAAAGTGAACA 2035
 QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTyr 660
 Db 2036 CCTCCAGTTCCAGGAACCTCCCACTAAGAAATCGTACTTCTCAGAGCTTCGGTTTGG 2095
 QY 661 SerGlnGlnSerSerArgProSerLeuValSerArgIleValLeuGlnSerGlnAspThrGlu 680
 Db 2096 TCTCAACAATCTTCTAGACCTCTTGAAAGAATGGTCTGTGAGAGCCAAAGATACAGAG 2155
 QY 681 AsnValProValThrLeuSerGlnGluAsnArgSerGlnGlyValValGlyPheGlnAla 700
 Db 2156 AATGTCCTCCAGTTACACTATCAAGAGAAACCGTTCTGAGAAAGAAAGTTGGTTTCAAGCC 2215
 QY 701 TyrIleValSerTyrPheArgIleGlyAlaHisIleTyrIleValPheIlePheLeuIleLeu 720
 Db 2216 TATTAAGATTTACTTGAAGCTGGTGTCTCACTGGAATGCTTCAATTTTCTTATTTCTCTA 2275
 QY 721 AsnThrAlaAlaGlnValAlaIleTyrValLeuGlnAspTyrTyrLeuSerTyrTyrAlaAsn 740
 Db 2276 AACACAGCAGCTCAAGGTGTCTTAATGTCTCAAGATTTGGTGGCTTCAATCTGGGGAAC 2335
 QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGluValLeuAsp 760
 Db 2336 AAACAAAGATATGCTAAATGTCACTGTAATGAGAGAGAAATGTAAACGAAAGCTAGAT 2395
 QY 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
 Db 2396 CTTAACTGGTACTTAGAAATTAATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2455
 QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
 Db 2456 GCAAGATCTCTATTTGGTATTTCAAGTCTTGTAACTCTTCAAACTTTGCAACAACAA 2515
 QY 801 MetPheGluSerIleLeuValAsnValProValLeuPheAspArgAsnProIleGlyArg 820
 Db 2516 ATGTTTGAATCAATTTTGAAAGCTCCGGATTTATCTTTTGATGAAATCAATAGGAAGA 2575
 QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisIleLeuAspAspLeuLeuProLeuThrPhe 840
 Db 2576 ATTTTAATCGTTTCTCAAAAGACATTTGACACTTGACATTTTGTGCGCGCTGACGTTT 2635
 QY 841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
 Db 2636 TTAGATTTTATCCAGACATTTGTCTACAAAGGTGTGGTGTCTCTGTGGCTGTGGCCGG 2695
 QY 861 IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuAlaArg 880
 Db 2696 ATTCCTTGGATCGCAATACCTTGGTTCCTCCCTTGAATCATTTTTCCTTCCGCGCA 2755
 QY 881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
 Db 2756 TATTTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTTCAACTCGGAGTCCAGTG 2815
 QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTyrThrIleArgAlaTyrLysAlaGlu 920
 Db 2816 TTTTCCACATTGTCATCTCTCTCCAGGGGCTGTGACCATTCGGGCGATACAAAGACAA 2875

QY 921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaIleTyrPheLeu 940
 Db 2876 GAGAGGTGTCAAGAACTGTTGATGACACACAGAGATTTAATTCAGAGGCTTGGTCTTGG 2935
 QY 941 PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
 Db 2936 TTTTGGACAAAGTCCCGCTGGTGGCTCCGCTGGATGGCATTGTGGCATGTGTTGTG 2995
 QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyValAlaGly 980
 Db 2996 ATCATGTTCCTTTGGTTCCTGATTTCTGGCAAAACCTTGATGTCGGGCGAGTTGGT 3055
 QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000
 Db 3056 TTGGCACTGCTCTTAAGCCCTCAGCTGATGGGAGATTTTCAAGTGTGTGTGCAAAAGT 3115
 QY 1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
 Db 3116 GCTGAAGTTGAATATGATGATCTCAGTAGAAAGGTCATTGAATACACAGACTTGAA 3175
 QY 1021 LysGluAlaProTyrGluTyrGluLysArgProProAlaTyrProHisGluGlyVal 1040
 Db 3176 AAAGAGACACTTGGGAATATCAGAAACGCCACACACAGCTGGCCCCATGAAGAGTG 3235
 QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
 Db 3236 ATTAATCTTGACAAATGTGAATTCATGTATACAGTCCAGGTGGGCTCTGTGTACTGAAGCAT 3295
 QY 1061 LeuThrAlaLeuIleLysSerGlnGluValGlyIleValAlaArgThrGlyAlaGly 1080
 Db 3296 CTGACAGACACTTAAATATCAACAAGAAAGTTGGCATTTGGAGAAACCGAGACTGGA 3355
 QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTyrIle 1100
 Db 3356 AAAATGTCCTCATCTCAGCCCTTTTGTGATTTGTTCAGAACCCGAAGATTAATTTGGATT 3415
 QY 1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
 Db 3416 GATTAAGATCTTGACAACTGAATTTGACCTTCACGATTTAAGGAAGAAATGCAATCATATA 3475
 QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
 Db 3476 CCTCAGGAACCTGTTTGTGTCTGAGCAAAAGAGAAAGAAACCTGATATCCCTTAATGAG 3535
 QY 1141 HisThrAspGluGluLeuTyrPheAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
 Db 3536 CACACGGATGAGAACTGTGAATGCTTTACAGAGGTACAACTTAAGAAACCATTTGA 3595
 QY 1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
 Db 3596 GATCTTCCTGGTAAATGGAATCTGATTAAGAGATCAGATCCAAATTTTGTGTGGA 3655
 QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
 Db 3656 CAAGAACAACGTGTGTGCTTGGCCAGGGCAATTTCTAGGAAAAATCAGATATGATTTAT 3715
 QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
 Db 3716 GATGAAGCGACGGCAAAATGTGATCCAGAACTGATGACTTAATCAAAAAAATCCGG 3775
 QY 1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
 Db 3776 GAGAAATTTGGCCACGTGACCGTGTCAACATTTGACACACAGATTTGAACCATTTTGTGAC 3835
 QY 1241 SerAspLysIleMetValLeuAspSerGlyValGluLysGluTyrTyrAspGluProTyrVal 1260
 Db 3836 ACCGACAGATATATGTTTATATTCAGGAACAACGAAAGATATGATGACCGATGTGT 3895
 QY 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlnLysValGlu 1280
 Db 3896 TTGCTGCATAAATTAAGAGAGCTTATTTTACAGATGTGTGCAACAACCTGGGCAAGCGAGA 3955

QY 1281 AaalaaleuThrglUthralaIySglnValIyRphelyArgAsnTyRProHisile 1300
 DB 3956 GCCGCTGCCCTCCTACACGAAACAGGAAACGGTACTTCAAAAGAAATTTATTCACATATT 4015
 QY 1301 GlnHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
 DB 4016 GGTCACTACGACCAATGCTGTACAAACATCTCAATGACAGCCCTGACCTTAATATT 4075
 QY 1321 PheGluThrAlaLeu 1325
 DB 4076 TTCGAGACGACACTG 4090
 RESULT 5
 ADH10624
 ID ADH10624 standard; DNA; 5833 BP.
 AC ADH10624;
 XX 11-MAR-2004 (first entry)
 DT 11-MAR-2004 (first entry)
 DE Human cancer-related polynucleotide, SEQ ID 14.
 XX Human cancer-related polynucleotide, SEQ ID 14.
 DE Human cancer-related polynucleotide, SEQ ID 14.
 XX Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.
 KW Homo sapiens.
 OS Homo sapiens.
 XX MO2003104404-A2.
 EN 18-DEC-2003.
 PD 18-DEC-2003.
 XX 05-JUN-2003; 2003MO-US017772.
 PF 06-JUN-2002; 2002US-0386651P.
 PR 06-JUN-2002; 2002US-0386651P.
 XX (AVALON PHARM INC.
 PA Ebner R;
 PI WPI; 2004-062332/06.
 XX Identifying agents that modulate the activity of cancer-related gene,
 PT useful for treating or diagnosing prostate cancer comprising contacting a
 PT compound with a cell containing a gene under conditions promoting
 PT expression of the gene.
 XX Claim 1; SEQ ID NO 14; 799p; English.
 PS The invention relates to identifying an agent that modulates the activity
 CC of a cancer-related gene. The method involves contacting a compound with
 CC a cell containing a gene that corresponds to a polynucleotide having a
 CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
 CC expression of the gene. The method is useful for identifying an agent
 CC that modulates the activity of a cancer-related gene. The polypeptides
 CC and antibodies of the invention are useful for treating and diagnosing
 CC cancer, preferably prostate cancer. It is also useful for screening
 CC assays for agents that are effective in reducing the activity of cancer-
 CC related genes. The present sequence represents a specific example of a
 CC cancer-related polynucleotide sequence.
 XX
 SQ Sequence 5833 BP; 1660 A; 1175 C; 1306 G; 1692 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 5833
 Score: 6785.00 Matches: 1324
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 99.9% Mismatches: 0
 Query Match: 12 Gaps: 0
 DB: 12 Gaps: 0
 US-09-976-858-42 (1-1325) x ADH10624 (1-5833)
 QY 1 MetLeuProValTyGlnGluValIySProAsnProLeuGlnAspAlaAsnLeuCySer 20

DB 116 ATGCTCCCGGTGATCCAGAGGTGAAGCCCAACCCGCTGACAGACGCAACATCTGCTCA 175
 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheValIleGlnHisIleArgArgLeuGlu 40
 DB 176 CGCGGTCTCTGTGGCTCAATCTCTGTTTAAATTTGGCAATTAACGGAGATTAGG 235
 QY 41 GluAspAspMetTyRSerValLeuProGluAspArgSerGlnHisLeuGlyValGluGluLeu 60
 DB 236 GAAAGTGAATATGATATTCAGTCTGCTCCAGAAACCGCTCACACACTTGAGAGAGATTG 295
 QY 61 GlnGlyPheTrpAspIySglnValIleuArgAlaGluAsnAspAlaGlnIySProSerLeu 80
 DB 296 CAAGGCTTCTGGATTAAGAAAGTTTAAAGCTGAGATGACGACAGAGCTTCTTTA 355
 QY 81 ThrArgAlaIleIleIleIySglnTyRTrpIySglnTyRLeuValIleGlyIlePheThrLeu 100
 DB 356 ACMAAGCAATCATMAAGTGTACGAAATCTTATTTAGTTTGGAAATTTTACGTTA 415
 QY 101 IleGluIleSerAlaIySglnValIleGlnProIlePheLeuGlyIleIleAsnTyRPh 120
 DB 416 ATTGAGAAAGTCCCAAGATTAATCCAGCCCATATTTTGGAAAAATTTATTAATTTT 475
 QY 121 GluAsnTyRAspProMetAspSerValAlaLeuAsnThrAlaTyRAlaTyRAlaThrVal 140
 DB 476 GAAATTTATGATCCCATGATTTCTGGCTTTGAACACAGCGTACGCCATATGCCAGGTTG 535
 QY 141 LeuThrPheCyThrLeuIleLeuAlaIleLeuHisIleLeuTyRPhetyRHisValGln 160
 DB 536 CTGACTTTTTCACCGCTCATTTTGGCTTATCTACGCTATCATTTATTTATCATCTTACG 595
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyRArgIySglnAlaLeuArg 180
 DB 596 TGCTGTGAATGAGGTTCAGAGTACCATGTGCCATTAATTAATTTATTCGAGAGCACTTCT 655
 QY 181 LeuSerAsnMetAlaMetGlyIySglnThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
 DB 656 CTTAGTAACATGCGCATGGGAGAGCAACACAGCGCAATGATCATCTGCTGTCCAT 715
 QY 201 AspValAsnIySPheAspGlnValThrValPheLeuHisIleLeuTrpAlaGlyProLeu 220
 DB 716 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACCTTCTGTGGCAGAGACACACTG 775
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCyLeuAlaGly 240
 DB 776 CAGCGATCGACGATCTGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 835
 QY 241 MetAlaValIleLeuLeuLeuLeuProLeuGlnSerCysPheGlyIySglnPheSerSer 260
 DB 836 ATGCAAGTTCTATCATCTCTCTGCTTGCAGAACTGTTTGGAGAGTTGTTTCATCA 895
 QY 261 LeuArgSerIySPheThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 DB 896 CTGAGAGATTAACATGCAATCTTTCAGGATCCAGATCCAGAGATCATGATGATGATGATGAT 955
 QY 281 ThrGlyIleArgIleIleIySglnMetTyRAlaTrpGlyIySglnPheSerAsnLeuIleThr 300
 DB 956 ACTGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1015
 QY 301 AsnLeuArgIySglnIleSerIySglnIleLeuArgSerSerCysLeuArgIySglnMetAsn 320
 DB 1016 AATTTGAGAAAGAGAGATTTCCAGAGTTCTGAGAAATCTCTGCTCAGGGGAGTGAAT 1075
 QY 321 LeuAlaSerPhePheSerAlaSerIySglnIleValIlePheValThrPheThrThrTyRVal 340
 DB 1076 TTGGCTTGTGTTTTCAGAGCAAGCAAAATCATCGTTGTGACCTTCAACCACTTACGCG 1135
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyRVal 360
 DB 1136 CTCTCTGCAAGTGTATACAGCCAGCCGCTGTTGCGAGTACCTGTATGAGGCT 1195
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
 DB 1196 GTGGGCTGAGAGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGCTGTCAAGAGCAATC 1255

QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
 Db 1256 GTCACATCCGAAAGATCCAGACCTTTTGTACTTGAATGAGATATCAACAGGCAACGCT 1315
 QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
 Db 1316 CAGCTGCCGTCAAGATGTGTAAAAAGATGTGTCAATGTGCAGATTTTAACTGCTTTTGGGAT 1375
 QY 421 LysAlaSerGluThrProThrIleuGlnGlyLeuSerPheThrValArgProGlyLeu 440
 Db 1376 AAGGATCAAGAACCCCACTTACAGGCTTTCTTTACTGTCAAGCTTGCGAATTG 1435
 QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValIleuGly 460
 Db 1436 TTAGCTGTGTGCGCCCGTGGAGAGAGAAAGTATCACTGTAAAGTCCGCTGCGG 1495
 QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
 Db 1496 GAATTGGCCCCCAAGTCAAGCGCTGTGCAGCGTGCATGGAAAGAAATGGCTTATGTCTCAG 1555
 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500
 Db 1556 CAGCCCTGGGTGTCTCGGAACTCTGAGAGTAAATATTATTGGGAAAGAAATATGAA 1615
 QY 501 LysGlnArgTyrGlyLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 Db 1616 AAGGAACGATGAAAAAGTCAATAAGCTTGTCCTGAAAGAAAGATTACAGCTGTG 1675
 QY 521 GlnAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
 Db 1676 GAGGATGGGATCTGACTGTGATAGAGATCGGGAAACCACTGTGTAGAGGCGAGAA 1735
 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
 Db 1736 GACGGGTAACTTGCAGAGACAGTGTATCAAGATGCTGAACATCTATCTCGAACAT 1795
 QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlyLeuLeuCysIleCysGln 580
 Db 1796 CCTCAGTGCAGTGAATGCGGAAGTTAGCAGACACTTGTGCACTGTGATTTGTGCA 1855
 QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
 Db 1856 ATTTTGCATGAGAAAGATCACAATTTTATGACTCATCACTGACAGTCTCAAGAGCTGCA 1915
 QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
 Db 1916 AGTCAGATTCTGATATTGAAGATGTGTAAATGTGTCAAGAGGGAATTACACTGAGTTTC 1975
 QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnLeuSerGlnGln 640
 Db 1976 CTAAATATCGTATGATTTTGGCTCCCTTTTAAAGAAAGATATAGAGAAAGTGAACA 2035
 QY 641 ProProValProGlyThrProThrLeuAlaGlnAsnArgThrPheSerGlnSerSerValTrp 660
 Db 2036 CCTCCAGTTCGAGAACTCCCACTAAAGAAATCGTAACTTCTCAAGAGCTTCGAGTTTG 2095
 QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680
 Db 2096 TCTCAACATCTTCTTGACCTTCCTTGAAGATGTGTCTGAGAGCCAAAGATACAGAG 2155
 QY 681 AsnValProValThrLeuSerGlnGlnAsnArgSerGlnGlyLysValGlyPheGlnAla 700
 Db 2156 AATGTCCTCAGTTACACTATCAAGAGAAACCGTTCGAAAGAAAGTGGTTTTTCAGGCG 2215
 QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
 Db 2216 TATTAAGAAATTACTTCAAGAGCTGTGTCTCACTGATTTCTCATTTTCTTATTTCTCCA 2275
 QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
 Db 2276 AACACTGACGCTCAGGCTGTCTATGTGCTTCAAGATTTGGGCTTTCATACAGGCGAAGC 2335

QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyLysAsnValThrGlyLysLeuAsp 760
 Db 2336 AAACAAAGTATGCTAAATGTCATCTGAATGAGAGAGAAATGTAAACGAGAAAGCTAGAT 2395
 QY 761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
 Db 2396 CTTAACGTGACTTGAAGATTTATTCAGGTTTAACTGTAAGCTACCGTCTTTTGGCATTA 2455
 QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
 Db 2456 GCAAGATCTATATGATTTGATTTCAAGTCCCTGTTAACTCTTGCAAAACCTTGCAACAAG 2515
 QY 801 MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspArgAspProIleGlyArg 820
 Db 2516 ATGTTTGATCAATCTGAAGCTCCGGATTTATCTTGTGTAGAAATCCAATAGAAAGA 2575
 QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisIleLeuAspAspLeuLeuProLeuThrPhe 840
 Db 2576 ATTTTAAATCGTTTCTCAAGACATTTGACACTTGGATGTGCTGTGCGCTGCGCGTTT 2635
 QY 841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValLysSerValAlaValAlaVal 860
 Db 2636 TTAGATTTCAATCAAGACATTTGCTACAGTGGTGTGTGCTGTGCGCTGCGCGG 2695
 QY 861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
 Db 2696 ATTCCTTGATCGCAATACCTTGTGTCCCTTGGAAATCAATTTTCAATTTTCTTGCGCA 2755
 QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900
 Db 2756 TATTTTGGAAACGTCAAGAGATGTAAAGCCCTGGAATCTTCAACTCGAAGTCAAGT 2815
 QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGln 920
 Db 2816 TTTTCCCACTTGATCATCTTCTCTCCAGGGGCTCTGAGACATCCGAGCATACAAACAGAA 2875
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 QY 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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 QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaTyrThrLeuAspAlaGlyGlnValGly 980
 Db 2996 ATCATCGTGTGCTTGGGTCCCTGATCTCGGAAAAACCTCGAGTCCGGGAGGTTGCT 3055
 QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
 Db 3056 TTGGCAGCTGCTTATGACCTCAAGCTCATGGGAGATGTTTCACTGTGTGTGTGCAAAAGT 3115
 QY 1001 AlaGlnValGlnAsnMetMetIleSerValGlnArgValIleGlnTyrThrAspLeuGln 1020
 Db 3116 GCTGAAGTTGAAGAAATGATGATCTCAAGTGAAGAAAGGTCATTTGAATACAGACCTTGAA 3175
 QY 1021 LysGlnAlaProTrpGlyTyrGlnLysArgProProProAlaTrpProHisGlnGlyVal 1040
 Db 3176 AAAGAGGACCTTGGGAATATCAGAAAGCCCAACCAAGAGCTGAGCCCATGAAGAGAGT 3235
 QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
 Db 3236 ATTAATCTTTGACAAAGTGAACCTTCAATGTAACATCCAGGGGCTCTGTGTACTGAAGCAT 3295
 QY 1061 LeuThrAlaLeuIleLysSerGlnGlyLysValGlyIleValGlyArgThrGlyValArg 1080
 Db 3296 CTGACAGCACTATTAATCAAGAAAGAGTTGGCATTTGTGGAAAGAACCGAAGCTGGA 3355
 QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGlnProGlyGlyLysIleTrpIle 1100
 Db 3356 AAAAGTCCCTCATCTCAGGCTTTTGTAGATTGTCAAGAACCGGAAGGTAAATTTGGATT 3415
 QY 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120


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DB 3416 GATTAAGATCTTACAACTGAATTTGACATTCACGATTTTAAAGAGAAAATGCAATCAATA 3475
QY 1121 PROGLINGUProValleuPheThrglyThrMetAglValAsnLeuAspProPheAsnGlu 1140
DB 3476 CCTCAGGAACCTGTTTGTTCCTGAGAACAAAGAGAAAACCTGATTCCTTTATATGAG 3535
QY 1141 HSTTAAspGluGluLeuThrAspAlaLeuGlnGluValGlnLeuLeuGluThrLeuGlu 1160
DB 3536 CACACGATGAGAACTGTGGATGCTTACAAAGAGTACAACTTAAAGAAACCAATTGAA 3595
QY 1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAspPheSerValGly 1180
DB 3596 GATCTTCCTGGTAAATGATCTGATTAAGCAATACGATTCACATTTTATGTTTGA 3655
QY 1181 GlnAglGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIle 1200
DB 3656 CAAGAACAACCTGTGTGCTTCCAGGCGCAATTCACAGGAAAATCAGATATTGATTAT 3715
QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
DB 3716 GATGAAGCGACGCAAAATGTGATTCAGAACTGATGATTAATCAAAAATAAAATCCGG 3775
QY 1221 GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleLeuAsp 1240
DB 3776 GAGAAATTTGCCCACTGACACCTGCTAACCAATTGCACACAGATTGACACCATTTTAC 3835
QY 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
DB 3836 AGCGCAAGATATATGTTTATGATTACAGGAAGACTGAAAGATATGATGAGCCGTATGT 3895
QY 1281 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyValGlu 1280
DB 3896 TTGCGCAAAATTAAGAAGCCTATTATTACAAAGATGTGCAACACTGGCAAGGACAGA 3955
QY 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
DB 3956 GCCGCTGCCCTCACGAAACACGAAACAGATATCTTCAAAAGAAATTTATCCACATAT 4015
QY 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
DB 4016 GGTTCACACTGACCAATGTTTACAAACACTTCATGACAGCCCTCGACCTTAATCTAT 4075
QY 1321 PheGluThrAlaLeu 1325
DB 4076 TTCGAGACGACCTG 4090

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RESULT 6
ADH10626
ID ADH10626 standard; DNA; 5862 BP.

XX ADH10626;
XX AC ADH10626;
XX DT 11-MAR-2004 (first entry)
XX DE Human cancer-related polynucleotide, SEQ ID 16.
XX KM Cancer-related gene; prostate cancer; cytosolic; human; gene; ds.
XX OS Homo sapiens.
XX PN WO2003104404-A2.
XX PD 18-DEC-2003.
XX PF 05-JUN-2003; 2003WO-US017772.
XX PR 06-JUN-2002; 2002US-0386651P.
XX PA (AVAL-) AVALON PHARM INC.
XX PI Ebner R;
XX

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DR WPI; 2004-062332/06.
PT Identifying agents that modulate the activity of cancer-related gene,
PT useful for treating or diagnosing prostate cancer comprising contacting a
PT compound with a cell containing a gene under conditions promoting
PT expression of the gene.
XX
XX PS Claim 1; SEQ ID NO 16; 79pp; English.
XX
XX CC The invention relates to identifying an agent that modulates the activity
XX of a cancer-related gene. The method involves contacting a compound with
XX a cell containing a gene that corresponds to a polynucleotide having a
XX sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
XX expression of the gene. The method is useful for identifying an agent
XX that modulates the activity of a cancer-related gene. The polypeptides
XX and antibodies of the invention are useful for treating and diagnosing
XX cancer, preferably prostate cancer. It is also useful for screening
XX assays for agents that are effective in reducing the activity of cancer-
XX related genes. The present sequence represents a specific example of a
XX cancer-related polynucleotide sequence.
SQ Sequence 5862 BP; 1645 A; 1208 C; 1328 G; 1681 T; 0 U; 0 Other;

```

Alignment Scores:
Pred. No.: 0 Length: 5862
Score: 6785.00 Matches: 1324
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.9% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 12 Gaps: 0

US-09-976-858-42 (1-1325) x ADH10626 (1-5862)

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QY 1 MetLeuProValTyrGlnValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
DB 116 ATGCGCCCGGTACAGAGAGGTGAGACCCGCTGCGAGAGCGCAACATCTGCTCA 175
QY 21 ArgValPhePheTyrPheLysProLeuPheLysIleGlyHisLysArgArgGlu 40
DB 176 GCGGTTCCTGCTGCTGCTCAATCCCTGTTTAAATGGCCAAATGAGATTAAG 235
QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlnGluLeu 60
DB 236 GAAGATGATATGATTCAGTCTGCTCCAGAAACCGCTCACAGCACTTGAGAGAGATTG 295
QY 61 GlnGlyPheTyrAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
DB 296 CAAGGTTCTGGATTAAGAAGATTTAAGACTGAGATGACGACAGAACCTTCTTTA 355
QY 81 ThrArgAlaIleIleLysCysTyrTyrLysSerTyrLeuValLeuGlyIlePheThrLeu 100
DB 356 ACMAAGCAATCATTAAGTGTACTGGAATCTTAATTAATTTTGGAAATTTTACGTTA 415
QY 101 IleGluGlnSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
DB 416 ATTGAGAAATGTCGCAAGTAAATCCAGCCATTTTGGGAAAATTTATTAATTTT 475
QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
DB 476 GAAATTAATGATCCCATGATTCGTGTGCTTGAACACAGCGTACGCTTATGCCAGGTG 535
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
DB 536 CTGACTTTTTCACGCTCATTTTGGCTTACTGATCATCTTAATTTTATTCACGTTAG 595
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
DB 596 TGTGCTGGAGTGAAGTTTACAGTACGATGCTGCTCATTAATTTATTCGAAAGCACTTGT 655
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlnIleValAsnLeuSerAsn 200
DB 656 CTTAGTAACATGCGCATGGGAGAGACACACAGCGCCAGATGATCAATCTGCTGCCAAT 715

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201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProLeu 220
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 Db 716 GATGTGAACAAGTTGATCAGAGGTGAACAAGTCTTACACTTCGTGGCAGAGCACACTG 775
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 221 GlnAlaIleAlaValThrAlaLeuLeuThrMetGlnIleGlyIleSerCysLeuAlaGly 240
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 Db 776 CAGGGCATGCAAGTGCCTCCCTACTGTGATGAGATGAGAAATACGTGCTGTGG 835
 |||||
 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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 Db 836 ATGGCAGTTCTAATCACTTCTCGGCCCTTGCAGAAAGCTGTTTTGGGAAGTGTTCATCA 895
 |||||
 261 LeuAspSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGlnValIle 280
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 Db 896 CTGAGGAGATAAACTGCACACTTTCACGGATGCCAGATCAGAACCTGATGAAGTTANA 955
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 281 ThrGlyIleArgIleIleLysMetTyrAlaTyrGlyLysSerPheSerAsnLeuIleThr 300
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 Db 1016 AATTGGAGAAAGAGAGATTTTCCAAAGATTCTGAGAAAGTTCCGGCTCAGGGGAGATGAT 1075
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 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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 Db 1076 TTGGCTTCCTTTTTCAGTCCAGCAAGCAAAATCATCGTGTGTGACCTTCCACCACTTACCGTG 1135
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 Db 1136 CTCTCTGGAGTGTGATCACGCCACGCCCGTGTGTGTGGCAGTGAACGCTGTATGGGAGCT 1195
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 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGlyLysValSerGlnAlaIle 380
 |||||
 Db 1196 GTGGCGCTACCGTTTACCTCTTCTTCCCTCAGCATTGAGAGGGGTGCAGAGGCAATC 1255
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 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGlnIleSerGlnArgAsnArg 400
 |||||
 Db 1256 GTTCAGATCCGAAGATCCAGACCTTTTGTCTACTTGATGAGATACACAGCGCAACCGT 1315
 |||||
 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTyrAsp 420
 |||||
 Db 1316 CAGCTGCCCTCAGATGTGTAAAGATGTGCATGTCCAGATTTTACTCTTTTGTGGAGT 1375
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 421 LysAlaSerGlnThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGlnLeu 440
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 Db 1376 AAGGATCATCAGACCCCAACTCATCAAGGCCCTTTTACTGTACGACTGGCGAATTG 1435
 |||||
 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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 Db 1436 TTAGCTGTGTGGCGCCCGTGGGAGCAGGGAAAGTCACTGTTAAGTCCGCTGGCG 1495
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 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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 Db 1496 GAATTGTGCCCCAAGTACGAGGCTGTGCAGCGTGTCAGAGAAATTCCTATGTGTCTCAG 1555
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 481 GlnProTyrValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500
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 Db 1556 CAGCCCTGGGTGTCTCGGGAACCTCAGAGAGTAAATTTTATTTCGGAAGAAATATGA 1615
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 501 LysGlnArgTyrGlnLysValIleLysValaCysAlaLeuLysLysAspLeuGlnLeu 520
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 Db 1616 AAGGAACGATATGAAAAAGTCATAAAGCTGTGTGCTCTGAAAAAGATTACAGCTGTGG 1675
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 521 GlnAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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 Db 1676 GAGGATGGGATGTGACTGTGATGAGAGATCGGGGAACCACTGTAGTGAAGGCGCAAGAA 1735
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 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspArg 560
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 Db 1736 GCACGGGTAAACCTTCCAGAGAGCAGTGTATCAAGATGCTGACATCTATCTCCGAGCAAT 1795
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 561 ProLeuSerAlaValAspAlaGlnValSerArgHisLeuPheGlnLeuCysIleCysGln 580

1796 CCTCAGTGCAGTGAAGAGCGAAGTTAGCAACACTGTTCGAACTGTGATTTTGTCA 1855
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 Db 581 IleLeuHisGlnLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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 Db 1856 ATTTTGCATGAGAGATCACAATTTTACTGACTCATCAGTTGCAGTTACTCAAGACTGCA 1915
 |||||
 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnGlnSerGln 640
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 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerValTyr 660
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 |||||
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 681 AsnValProValThrLeuSerGlnGlnLysAsnArgSerGlnGlyLysValGlyPheGlnAla 700
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 Db 2396 CTTAAGTGTACTTGAAGATTTATTCAGGTTTAACTGATGACGTTCTTTTGGCATA 2455
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 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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 Db 2456 GCAGATCTCTAATGTGATTTCTACCGTCTGTGTAACCTTCAAACTTGTGACAAACAA 2515
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 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuProLeuThrPhe 840
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 Db 2576 ATTTTAATCTGTTTCCAAAGACATTTGACACTTGGATGATTTGCTGCGCTGACGTTT 2635
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 841 LeuAspPheIleGlnThrLeuLeuGlnValAlaGlyValaSerValAlaValAlaVal 860
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 Db 2756 TATTTTTCGAAACCTCAAGAGATGTGAAGCCCTCGAATCTCAACACTCGAGTCCAGTG 2815
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 921 GlnArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaIleThrPheLeu 940

Db 2876 GAGAGGTGTCAGGAACCTGTTGATGACACACAGATTACATTCAGAGGCTTGTTCTTG 2935
 Qy 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
 Db 2936 TTTTGGACAAACGCTCCGCTGCTGCGCCGCTCGGATGCACTGTGTCATGTTTGTGC 2995
 Qy 961 IleIleValAlaPheGlySerLeuIleLeuAlaIleThrLeuAspAlaGlyGlnValGly 980
 Db 2996 ATCATCTGCTGCTTGCGGCTCCGTGATTCCTGGCAAAACCTCGATCCCGGAGGTTGGT 3055
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 Db 3356 AAGAGTCCCTATCTCAGCCCTTTTATGATTTGTCAAGCCGAGAGGTAATTAATTTGGATT 3415
 Qy 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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 Qy 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140
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 Db 4076 TTGAGACAGCACTG 4090
 Db
 RESULT 7
 ADW14765
 ID ADW14765 standard; cDNA; 4078 BP.
 XX
 AC ADW14765;
 XX
 DT 07-APR-2005 (first entry)
 DE Tumor-associated antigenic target TAT425 cDNA clone DNA340411.
 XX
 KW Tumor-associated antigenic target; TAT425; cancer; neoplasm; cytosolic;
 XX renal tumor; uterus tumor; prostate tumor; pancreas tumor; gene; ss.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FH CDS 8..3985
 FT /tag=a
 FT /product="TAT425"
 FT /transl_except=" (pos:2630..2632,aa:Phe)
 XX
 PN MO200503154-A2.
 PD 13-JAN-2005.
 XX
 PF 02-JUL-2004; 2004WO-US021353.
 XX
 PR 02-JUL-2003; 2003US-0484959P.
 XX
 PA (GENE) GENENTECH INC.
 XX
 PI Ashkenazi A, Calms B, Dowd P, Frantz G, French D, Gonzalez L;
 PI Polakis P, Smith V, Wolf B, Wu TD, Zhang Z;
 XX
 DR MPI: 2005-091764/10.
 DR P-PSDB; ADW14772.
 XX
 PT New Tumor-associated Antigenic Target polypeptides useful for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer or
 PT tumor.
 XX
 PS Claim 1; SEQ ID NO 3; 141bp; English.
 XX
 CC The present sequence is that of cDNA clone DNA340411 encoding novel tumor
 CC associated antigenic target polypeptide TAT425. TAT polypeptides have
 CC been identified ADW14770-ADW14776 whose expression is upregulated in
 CC particular tumor tissues. Tissue expression profiling using GeneExpress
 CC indicated that TAT425 is upregulated in kidney tumor and prostate tumor
 CC tissues as compared to the corresponding healthy tissues. Upregulation in
 CC prostate tumor tissue was confirmed by quantitative analysis of TAT mRNA
 CC expression, and results were confirmed by gene expression profiling in
 CC silico (GEPIS) analysis which also indicated upregulation in uterus tumor
 CC and pancreas tumor tissues. The TAT polypeptide may comprise the full-
 CC length polypeptide, or the extracellular domain, and may be fused to a
 CC heterologous polypeptide such as an epitope tag, or the Fc region of an
 CC immunoglobulin. TAT polypeptides of the invention, and their encoding
 CC nucleic acids, provide targets for the diagnosis and therapy of cancer.
 XX
 SQ Sequence 4078 BP; 1141 A; 839 C; 979 G; 1119 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 4078
 Score: 6781.00 Matches: 1324
 Percent Similarity: 99.94 Conservative: 0

Best Local Similarity: 99.9% Mismatches: 1
Query Match: 99.9% Indels: 0
DB: 14 Gaps: 0

US-09-976-858-42 (1-1325) x ADM14765 (1-4078)

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QY 21 ARGVal1PhePheTrpTrpLeuAsnProLeuPheLys11eGly1HisLysArgArgLeuGlu 40
DB 68 CGCGGTCTCTCGTGGCTCAATCCCTTGTTTAAATTTGGCCATTAACGAGATTAGAG 127
QY 41 GluAspAspMetTyrSerVal1LeuProGluAspArgSerGlnHisLeuGly1GluGluLeu 60
DB 128 GAAAGATGATATGATATTCAGTGGCTGCCAAGAACCGCTCAAGACCTTGAGAGAGATTG 187
QY 61 GInGlyPheTrpAspLysGluVal1LeuArg1aGluAsnAspAlaGlnLysProSerLeu 80
DB 188 CAAGGCTTCGGATTAAGAAAGTTTMAAGCTGAGAAATGACGCACAGAAAGCCTTCTTAA 247
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QY 141 LeuThrPheCyThrLeu1leuAla1le1leuHis1leuThrPheTyrHisValGln 160
DB 428 CTGACTTTTGGACGCTCAATTTGGCTATACGACATCACTTAATTTTATCAAGTTCAG 487
QY 161 CyBALaG1YMeCArgLeuArgVal1a1aMetCyHis1aMet11eTyrArgLysAlaLeuArg 180
DB 488 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGACCTTGT 547
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGln11eVal1aAsnLeuSerAsn 200
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QY 201 AspValAsnLysPheAspGlnVal1ThrVal1PheLeuHis1PheLeuThrAlaGlyProLeu 220
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QY 221 GlnAla1le1a1aVal1ThrAlaLeuLeuTyrMetGlu11eGly11eSerCySerLeu1aGly 240
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QY 241 MetAlaVal1leu11e1leLeuLeuProLeuGlnSerCyPheGlyLysLeuPheSerSer 260
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QY 321 LeuAlaSerPhePheSerAlaSerLys11e1leVal1PheVal1ThrPheThrThrTyrVal 340
DB 968 TTGGCTTCGTTTTCAGTGCAGCAAAATCATGCTGTGTGTGACCTTCAACCACTTACG 1027

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QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrVal1ArgProGlyGluLeu 440
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QY 441 LeuAlaVal1a1aGlyProVal1a1aGlyLysSerSerLeuLeuSerAlaVal1leuGly 460
DB 1328 TTACGCTGTGTGCGCCCGTGGAGACAGGAAATCATCACTGTTAAGTCGCTCGGG 1387
QY 461 GluLeuAlaProSerHisGlyLeuVal1SerVal1HisGlyArg11eAlaTyrValSerGln 480
DB 1388 GAATTTGGCCCCAAGTACAGGCGCTGTGACCGTGCAGAGAAAGATTCATGTGTCTCAG 1447
QY 481 GlnProTrpVal1PheSerGly1ThrLeuArgSerAsn11eLeuPheGlyLysLysTyrGlu 500
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QY 501 LysGluArgTyrGluLysVal11eLysAlaCyBALeLysLysAspLeuGlnLeuLeu 520
DB 1508 AAGGAACATAGAAAGAAAGTCAATAAGCTTGTGCTGAAGAAAGATTTACAGCTGTTG 1567
QY 521 GluAspGlyAspLeuThrVal11eGlyAspArgGly1ThrThrLeuSerGly1GlyGlnLys 540
DB 1568 GAGGATGGTGAATCTGACTGTGATAGAGATCGGGGAAACACCGCTGAGTGAGGAGAA 1627
QY 541 AlaArgVal1aAsnLeuAlaArgAlaVal1TyrGlnAspAlaAsp11eTyrLeuLeuAspAsp 560
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 QY 1321 PheGlnThrAlaLeu 1325
 DB 3968 TTCAGACAGCACTG 3982
 DB 3968 TTCAGACAGCACTG 3982
 RESULT 8
 AA230078
 ID AA230078 standard; cDNA; 4231 BP.
 AC AA230078;
 XX
 DT 26-JAN-2000 (first entry)
 DE cDNA encoding a human MPR-related ABC transporter designated MOAT-B.
 KW Human; MPR-related ABC transporter; MOAT protein; MOAT-B;
 KW MOAT mediated transport; anticancer drug sensitivity;
 KW transporter mediated cellular efflux; anticancer; ss.
 OS Homo sapiens.
 OS
 FT Key Location/Qualifiers
 CDS 116..4093

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FT      /tag= a
FT      /product= "MOAT-B"
FT      /transl_except= (pos: 1715..1717, aa: Pro)
FT      /transl_except= (pos: 3568..3568, aa: Arg)
FT      /note= "MPR-related ABC transporter"
PN      WO9949735-A1.
XX      07-OCT-1999.
XX      26-MAR-1999; 99WO-US006644.
XX      27-MAR-1998; 98US-0079759P.
XX      PR 03-AUG-1998; 98US-0095153P.
XX      PA (FOX-) FOX CHASE CANCER CENT.
XX      PI Krub G, Lee K, Belinsky M, Bain L;
XX      DR WPI, 1999-610812/52.
XX      DR P-PSDB; AAY43541.
XX      PT New transporter gene useful for screening for anti-cancer drugs.
XX      PS Claim 1; Page 130-131; 153pp; English.
XX      CC The present sequence encodes a human MPR-related ABC transporter (MOAT)
XX      CC protein, designated MOAT-B. The protein comprises a multi-domain
XX      CC structure including a tandem repeat of nucleotide binding folds appended
XX      CC C-terminal to a hydrophobic domain, having Walker A and B ATP binding
XX      CC sites and several potential membrane spanning domains. The MOAT nucleic
XX      CC acids are useful for screening a test compound for inhibition of MOAT
XX      CC mediated transport, indicated by restoration of anticancer drug
XX      CC sensitivity, which in turn causes a reduction of transporter mediated
XX      CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
XX      CC probes to detect the presence or expression of genes encoding MOAT
XX      CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating
XX      CC MOAT proteins
XX      SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other:

Alignment Scores:
Pred. No.: 0 Length: 4231
Score: 6779.00 Matches: 1323
Percent Similarity: 99.9% Conservative: 1
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 99.9% Indels: 0
DB: 2 Gaps: 0

US-09-976-858-42 (1-1325) x AA230078 (1-4231)
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QY      21 ArgValPhePheTrpIleuAsnProLeuPheIleGlyHisIleArgArgLeuGln 40
DB      176 CCGGCTTCTTCGCGGTCAATCCCTGTTTAAATGGCCATTAACGAGATTAGAG 235
QY      41 GluAspAspMetTyrSerValIleuProGluAspArgSerGlnHisIleuGlyGluGlu 60
DB      236 GAGAGATGATATGATTCAGTGTGCGCAGAAACCGCTCAACGACCTTGAGAGGAGTGG 295
QY      61 GlnGlyPheTrpAspArgGluValIleuArgAlaGluAsnAspAlaGlnIleuProSerIleu 80
DB      296 CAAGGGTTCTGGAGTAAAGAGTTTAAAGCTGAGAAATGACGCAAGAGCCCTTCTTA 355
QY      81 ThrArgAlaIleIleIleCysTyrTrpIleuValIleuGlyIlePheThrLeu 100
DB      356 ACAAGGCAATCATTAAGTCTTACTGGAATCTTATTAGTTTGGGAATTTTACGTTA 415
QY      101 IleGluSerAlaIleValIleGlnProIlePheLeuGlyIleIleAsnTyrPhe 120

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QY      161 CysAlaGlyMetArgLeuAsnArgValAlaMetCysHisMetCileTyrArgIleValLeuArg 180
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QY      221 GlnAlaIleAlaValThrAlaLeuLeuThrPheGlnIleGlyIleSerCysLeuAlaGly 240
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DB      896 CTGAGAGCTGAACACGCAACTTTCACGATGCGAGATGACAGACCATGAATGAATTTA 955
QY      281 ThrGlyIleArgIleIleIleLeuMetTyrAlaTrpGluIlePheSerAsnLeuIleThr 300
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QY      301 AsnLeuArgIleGlyIleIleSerIleLeuArgSerSerCysLeuArgIleMetAsn 320
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QY      321 LeuAlaSerPhePheSerAlaSerIleIleIleValIlePheValIlePheThrThrTyrVal 340
DB      1076 TTGGCTGTTTTCAGTGAAGCAAAATCATCGTGTGTCACCTTACCACTTACGTCG 1135
QY      341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValIleThrLeuTyrGlyAla 360
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DB      1196 GTGGCGCTGACGCTTACCTCTTCTCCCTGACCATTTGAGAGGCTGACAGCAATC 1255
QY      381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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QY 901 PheSerHlaLeuSerSerSerLeuGlnGlyLeuTyrThrIleArgAlaTyrLysAlaGln 920
Db 2816 TTTTCCACTGTGTACTTCTCTCCAGGGGCTCTGACATCCGGGCAATCAACACAGA 2875
QY 921 GluArgCysGlnGluLeuPheAspAlaHlaGlnAspLeuHlaSerGluAlaTyrPheLeu 940
Db 2876 GAGAGGTGCAGAACTGTTGATGACACAGATTTACATTCAGAGGCTGTGTTCTTG 2935
QY 941 PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
Db 2936 TTTTGGACAGCTCCCGCTGTGCGCGTCCGTGATGCTCATGCTGCTGCTGCTGCTGCT 2995
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyValValGly 980
Db 2996 ATCATCGTTGCTTTGGGCTCTGATTTCTGCAAAACCTTGATCCCGGAGAGTTGGT 3055
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000
Db 3056 TTGGCACTGCTCAATGCCCTCAGCTCAGTGGGAGTGTTCAGTGTGTGTCGACAAAGT 3115
QY 1001 AlaGluValGluAsnMetMetIleSerValGluValGluValIleGlnTyrThrAspLeuGln 1020
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QY 1021 LysGluAlaProTPrGluTyrGluLysArgProProAlaTyrProHlaGluGlyVal 1040
Db 3176 AAAGAAACCTTGGGAATATCAAGAACGCCCAACACAGCTGGCCCATTAAGAGAGT 3235
QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHla 1060
Db 3236 ATTAATCTTGAACAATGTGAATCTCATGTATGATGTCAGAGTGGGCTCTGGTATCTGAAGCAT 3295
QY 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
Db 3296 CTGACAGACCTCATTAATATCAACMAAAAGTTGGCATTTGGGAAAGAACCGAGCTGGA 3355
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTyrIle 1100
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QY 1101 AspLysIleLeuThrThrGluIleGlyLeuHlaAspLeuArgLysLysMetSerIleIle 1120
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QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140
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Db 3536 CACAGAGATAGAGAACTGTGAAATCTCTTCAAGAGGTACCACTTAAAGAAACCAATTGAA 3595
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QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220

QY 281 ThrGIleArgIleIleYseMetTyrAlaTPGIuLYseSerPheSerAsnLeuIleThr 300
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 QY 321 LeuAlaSerPhePheSerAlaSerLYsIleIleValPheValThrPheThrThrTYrVal 340
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 DB 1316 CAGCTCGGTCAGATGGTAAGTAAGATGGCATGTGCAGGATTTTACGTCTTTTGGAGT 1375
 QY 421 LYsAlaSerGIuThrProThrLeuGLYGLYLeuSerPheThrValArgProGLYGLYLeu 440
 DB 1376 AAGGATCAGAGACCCCAACTCTACAGGCTTTCTTACTGTCAAGCTGCCAATGG 1435
 QY 441 LeuAlaValValGLYProValGLYAlaGLYLYseSerLeuLeuSerAlaValLeuGLY 460
 DB 1436 TTAGCTGTGTGTGCGCCCGTGGAGCAGGAGATCATCATCTTAAAGTCCGTGTCGGG 1495
 QY 461 GluLeuAlaProSerHisGLYLeuValSerValIleGLYArgIleAlaTYrValSerGIu 480
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 QY 481 GluProTrpValPheSerGLYThrLeuArgSerAsnIleLeuPheGLYLYsIleTYrGLY 500
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 QY 501 LYsGIuArgTYrGLYLYsValIleLYsAlaCysAlaLeuLYsAspLeuGLYLeuLeu 520
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 QY 581 IleLeuHisGLYLYsIleIleThrIleValThrHisGLYLeuGLYTYrLeuLYsAlaIle 600
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 DB 1976 CTAATAATCTGGATATGATTTTGTGCTCCCTTTAAAGAGATTAATGAGGAAAGTGAACA 2035

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 QY 921 GluArgCysGIuGLYLeuPheAspAlaHisGLYAspLeuHisSerGIuAlaTrpPheLeu 940
 DB 2876 GAGAGGTGTCAAGAACTGTTGATGACACACAGATTTTACATTTCAAGAGGCTGTGTTCT 2935
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QY 1121 ProGluGluProValLeuPheThrGlyIuTrMetArgLysAsnLeuAspProPheAsnGlu 1140
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QY 1141 HisThrAspGluGluLeuTrpAsnAlaLeuGluGluValGluLeuIleGluThrIleGlu 1160
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QY 1321 PheGluThrAlaLeu 1325
DB 4076 TTCGAGACGACCTG 4090

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RESULT 10
 ABV75072
 ID ABV75072 standard; DNA; 4231 BP.
 XX
 AC ABV75072;
 XX

DT 19-FEB-2003 (first entry)
 XX
 DE Human DevG4 homologue protein encoding DNA.
 XX
 KW Protein disulfide isomerase; DevG20; ABC transporter; DevG4; DevG22;
 KW anorectic; immunomodulator; antidepressant; antidiabetic; hypotensive;
 KW antitumor; antileukemic; antiparasitic; antipneumonic; antipneumonic;
 KW litholytic; hepatotropic; cytosolic; neuroprotective; gene therapy;
 KW transgenic; human; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 115..4092
 FT /tag=a
 FT /product="DevG4 homologue protein"
 FT
 FN WO200279238-A2.
 FN
 XX
 PD 10-OCT-2002.
 PD
 PF 28-MAR-2002; 2002MO-BP003540.
 PF
 XX
 PR 02-APR-2001; 2001EP-00108315.
 PR
 XX 01-JUN-2001; 2001EP-00113419.
 XX
 PA (DEVE-) DEVELOPMENTAL BIOLOGICALS FORSCH.
 PI Eulenberger K, Bremer G, Ciosek T, Haeder T, Steuernagel A;
 XX
 DR WPI; 2003-067420/06.
 DR
 XX P-PSDB; ABB82645.
 XX
 PT New protein disulfide isomerase and ABC transporter nucleic acids or
 PT polypeptides, useful for diagnosing, treating or preventing obesity,
 PT hypertension, heart disease, hypercholesterolemia, osteoarthritis,
 PT gallstones or cancer.
 PT
 XX
 PS Claim 2; Fig 9C; 99p; English.
 PS
 CC The invention relates to pharmaceutical composition comprising carrier,
 CC diluents and/or adjuvants, with any of: (a) a nucleic acid molecule of
 CC the protein disulfide isomerase (DevG20) or ABC transporter (DevG4 or
 CC DevG22) gene family; (b) a polypeptide encoded by (a); (c) a fragment or
 CC variant of (a) or (b); or (d) an antibody, an aptamer or another receptor
 CC recognizing (a) or (b). The composition is useful for manufacturing an
 CC agent for detecting and/or verifying, diagnosing, treating, alleviating
 CC or preventing a metabolic disorder, e.g. obesity, adipositas, eating/body
 CC weight disorders, cachexia (wasting), pancreatic dysfunction (diabetes
 CC mellitus), hypertension, arteriosclerosis, coronary artery disease (CAD),
 CC coronary heart disease, hypercholesterolemia, dyslipidemia,
 CC osteoarthritis, gallstones, cancer (cancer of the reproductive organs),
 CC sleep apnea, disorders related to ROS production and neurodegenerative
 CC diseases in cells, cell masses, organs and/or subjects. The inhibitors,
 CC modulators or agents identified above are useful for treating, preventing
 CC or alleviating the diseases mentioned. The nucleic acid molecule of
 CC DevG20, DevG4 and/or Dev is also useful for preparing a non-human animal
 CC which over- or underexpresses the DevG20, DevG4 and/or Dev gene product.
 CC The present sequence represents a DNA encoding a human DevG4 homologue
 CC protein, a ATP-binding cassette, sub family C (CFTR/MRP), member 4, also
 CC referred to as ABCC4 and MPR4 (Gen Bank Accn No. NM_005845)
 CC
 SQ Sequence 4231 BP; 1170 A; 894 C; 1016 G; 1151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 4231
 Score: 6779.00 Matches: 1323
 Percent Similarity: 99.9% Mismatches: 1
 Best Local Similarity: 99.8% Indels: 0
 Query Match: 99.9% Gaps: 0
 DB:

US-09-976-858-42 (1-1325) x ABV75072 (1-4231)

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 QY 21 ArgValPhePheTrpIleuAanProLeuPheValIleGIYHISlySArgrgleuGIu 40
 Db 176 CCGCGTCTCTTGGGGCTCAATCCCTGTTTAAATGGCCATMAACGAGATTAAGAG 235
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 Db 236 GAAAGATGATATGTATTCAGTGTCTGCCAAGAACCGCTCAGACACCTTGGAGAGGAGTGG 295
 QY 61 GInGIyPheTrpAspIyGIuValIeuAArgAlaIuAanAspAlaGIuIySProSerLeu 80
 Db 236 CAAAGGCTTGGGATTAAGAAAGTTTAAAGCTGAGATGACGACAGAACCTTCTTTA 355
 QY 81 ThrArgAlaIleIleIySPeTyTrpIySPeTyLeuValIleuGIyIlePheThrLeu 100
 Db 356 ACAAGAGCAATCATAAAGTGTACTGGAAATCTTAATTTAGTTTGGGAATTTTACGTTA 415
 QY 101 IlegIuIuSerAlaIyValIleGIuProIlePheLeuGIyIyIleAanTyPhe 120
 Db 416 ATTTGAGAAAGTGCAGAAAGTAAATCCAGCCCATATTTTGGGAAAATTTATTAATTA 475
 QY 121 GluAanTyPheProMetAapSerValAlaIeuAanThrAlaTyPheAlaThrVal 140
 Db 476 GAAATTTATGATCCCATGGATTTCTGTGGCTTGAACACAGCGTACCGCTTACGACGG 535
 QY 141 LeuThrPheCyThrLeuIleleuAlaIleuHISlySArgrPheTyPheValGIu 160
 Db 536 CTGACCTTTTGGACCGCTCATTTTGGCTAATCGCATCACTTAATTTTATCACGTTGAG 595
 QY 161 CySAIaGIyMeArGIeuaArgValAlaIeMetCySHISMetIleTyPheArgValAlaIeuArg 180
 Db 596 TGTGTGGGATGAGGTTCAGAGTACGATGTCACATATGATTTATTCGAGAGCACCTTCGT 655
 QY 181 LeuSerAanMetAlaMeGIyIySPeTyPheThrThrGIuIleValIaIuAanLeuSerAan 200
 Db 656 CTTAGTAAATGATGCGCATGGGAGAAAGACACACAGGCGCATATGTCATCTGTCTCAT 715
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 Db 716 GATGTGAACAATTTGATTCAGGTGACAGTGTCTTAACCTTCTGTGGGACAGACACAG 775
 QY 221 GInAlaIleAlaValIleThrAlaIeuLeuTyPheGIuIleGIyIleSerCySAIaGIy 240
 Db 776 CAGGCGATCGCAGTACGTGCCCTACTGTGATGAGATGAGAAATTCGTGCTGTGGG 835
 QY 241 MetAlaValIleuIleIleuLeuProLeuGIuIySPeTyPheGIyIyIleuPheSerSer 260
 Db 836 ATGGCAGTCTTAATCATCTGTCTGTGCCCTTGGCAAGCTGTTTGGGAAGTGTTCATCA 895
 QY 261 LeuAArgSerIySPeThrAlaThrPheThrAspAlaArgIleArgThrMeAanGIuValIle 280
 Db 896 CTGAGAGAGTAAACCTGCACTTTCACGATGCGACAGATGACAGACCATGAATGAATTA 955
 QY 281 ThrGIyIleArgIleIleIySPeTyPheValIlePheGIyIySPeSerAanLeuIleThr 300
 Db 956 ACTGTATTAAGATATATAAAATGTACGCTGGGAAAAGTCAATTTCAATCTTAATACC 1015
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 Db 1376 AAGGATGAGAGACCCCACTCTACAAAGCCCTTCTTACGTGACAGCTGGCAATGG 1435
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 Db 1856 ATTTGCAATGAGAGATCAAAATTTAGTCACTATCAGTTGCACTACCTCAAACTGCA 1915
 QY 601 SerGIuIleuIleLeuIyAapGIyIySPeValIleGIuIyIySPeTyPheThrGIuPhe 620
 Db 1916 AGTCAGATTTCTGATTTTAAAGATGTGTAATGTGTGCAAGAGGAGCTTACCTAGATTC 1975
 QY 621 LeuIySPeGIyIleAapPheGIySerLeuLeuIyIyAapAanGIuIySerGIuGIu 640
 Db 1976 CTAATAATCTGTATATGATTTTGGCTCCCTTTTAAAGAGATTAATGAGAAAGTGAACA 2035
 QY 641 ProProValProGIyThrProThrLeuAArgAanArgThrPheSerGIuSerSerValIle 660
 Db 2036 CCTCAGTTCAGAGAACTCCCACTAAAGATGTATCTTCTCAGACTCTTCGCTTGG 2095
 QY 661 SerGIuIySPeSerArgProSerIleuIyAapGIyAlaIeuGIuIySerGIuAapThrGIu 680
 Db 2096 TCTCAACATCTTCTAGACCTCTCTTGAAGATGTGTCTGAGAGGCCAAGATACAGAG 2155
 QY 681 AenValIleProValIleLeuSerGIuIyAanAArgSerGIuIyIySPeValIlePheGIuAla 700
 Db 2156 AATGTCCAGTTTACATATCAGAGAGAAACCTTCTGAAAGAAAGTGTGTTTACAGGCC 2215
 QY 701 TyPheAanTyPheAArgAlaGIyAlaHISlyIleValIlePheIlePheLeuIleLeu 720
 Db 2216 TATAGATTTACTCAGAGCTGTGTCTCACTGATGTCTTCAATTTCTTATTTCTCTTA 2275
 QY 721 AenThrAlaIleGIuIleValIleAlaTyPheValIleuGIuAapTrpIlePheSerTyPheAlaAan 740

Db	2276	AAACATGAGCTCAGGTTGCTTATGTGCTTCAAAATTTGTTGCTTCACTACCTGGGCAAC	2335
QY	741	LYSGINserMetLeuAsnValThrValAsnGlyGlyAsnValThrGluLeuAsp	760
Db	2336	AAACAAAGTATAGCTAAATGATCACTGTAAATGAGAGAGAAATGTATACGAAACCTGAT	2395
QY	761	LeuAsnTrpPylLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle	780
Db	2386	CTTAACGTGACTTAGGAATTTATTCAGGTTTAACTGACGTTCCTTTTGGCAT	2455
QY	781	AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys	800
Db	2456	GCAAGATCTCTATTGGTATCTCAAGCTCTGTATTAACCTTCACAAACCTTGCACAAACAA	2515
QY	801	MetPheGluSerIleLeuValAlaProValLeuPheAspArgAsnProIleGlyArg	820
Db	2516	ATGTTTGAGTCAAATTCGAAAGCTCCGGTATATTCCTTGTATGATGAAATCCAAATGGAAGA	2575
QY	821	IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe	840
Db	2576	ATTTTAATTCGTTTCTCCAAAGACATTGGACACTTGATGATTTTGCTGGCTACGTTT	2635
QY	861	LeuAspPheIleGlnThrLeuLeuGlnValGlyValValSerValAlaValAlaVal	860
Db	2636	TTAGATTTCATCCAGACATTCCTCAAGATGGTGGTGGTCTCTGGGGCTGGCCGTG	2695
QY	861	IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg	880
Db	2686	ATTCCTTGATCGCAATACCTTGGTTCCTTGGAATCATTTTTCATTTTCTTCGGGCA	2755
QY	881	TyrPheLeuGlnThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal	900
Db	2756	TATTTTGGAAACCTCAAGAGATGTGAAGCGCCTGAATCTACACTCGAGTCCAGTG	2815
QY	901	PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpTrpIleArgAlaTyrLysAlaGlu	920
Db	2816	TTTTTCCACTGTCAATCTTCTCTCCAGGGCGCTGTGACATTCGGGCAATCAAGACAA	2875
QY	921	GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluValATrPheLeu	940
Db	2876	GAGAGGTGTCAAGAACTGTGTGATGCAACACAGAGATTACATTCAGAGGCTGTGGTCTG	2935
QY	941	PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal	960
Db	2936	TTTTTGAACAACGTCCCGCTGGTTCGCCGTCGTGATGCAATGTCATGTGGCATGTTTCTC	2995
QY	961	IleIleValAlaPheGlySerLeuIleLeuAlaLysTrpLeuAspAlaGlyValGly	980
Db	2996	ATCATCTGTGCTTTGGGTCTCCCTGATTTTGGCAAAAACCTCGAGATCCGGGCAAGTGTGT	3055
QY	981	LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer	1000
Db	3056	TTGGCACTGTCTATAGCCCTCAACGCTCAAGGGAGTTTCAGTGGTGTGTGCAAAAGT	3115
QY	1001	AlaGluValAlaAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu	1020
Db	3116	GCTGAAGTTGGAATATATATGATCTCAGTAGAAAGGTCATTGAATACACAGACTTGA	3175
QY	1021	LysGluAlaProTrpGluTyrGlnLysArgProProAlaATrPProHisGluGlyVal	1040
Db	3176	AAAGAGACACCTTGGGAATATACAGAAAGCCCAACACAGCCTGGCCCCCAATGAAGAGTG	3235
QY	1041	IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis	1060
Db	3236	ATTAATCTTGTGAACAATGTGAACCTTCACTGACGTCCAGGTGGCCCTCTGTACTGAAGAT	3295
QY	1061	LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyValaGly	1080
Db	3286	CTGACAGCACTCATTAATCACAGAAAGGTTGGCATTTGTGGAAAGAACCGAGCTGGA	3355
QY	1081	LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle	1100

Db	3356	AAAAGTCCCTCAGCTCAGCCCTTTTGAAGTTGACAGAACCCCGAGGTAATAATTTGGATT	3415
Qy	1101	AspArgyleuThrThrGluIleGlyLeuHisAspLeuArgIleValMetSerIleIle	1120
Db	3416	GATAGAGATCTTGACACTGAGAAATGGACTTCACACATTTAAGAAAGAAATGTCATCATATA	3475
Qy	1121	ProGlnGluProValLeuPheThrGlyThrMetArgIleAsnLeuAspProPheAsnGlu	1140
Db	3476	CCTCAGGACCTGTTTTTTGTTCACTGGAACATATGAGAAAAACCTGGATTCCTTTAAGAG	3535
Qy	1141	HisThrAspGluGluLeuThrPheAsnAlaLeuGlnGluValGlnIleuIleuValIleGlu	1160
Db	3536	CACACGAGATGGAGAACTGTGGAAAGCTTTCACAGAGGTATCACTTTAAAGAAACCATTTGAA	3595
Qy	1161	AspLeuProGlyIleMetCAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly	1180
Db	3596	GATCTTCTCGTTAAATATGATACGTATTTAGCAGAAATCAGAGATCCATTTTAGTTGGA	3655
Qy	1181	GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgIleAsnGlnIleLeuIleIle	1200
Db	3656	CAAGACACAACTGGTGTCTCTTCCAGGGGCAATTTCTCAGAAATAATCAGATATGATTATTT	3715
Qy	1201	AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnIleValIleArg	1220
Db	3716	GATAGAGGAGGGGCAAAATGGATATCCAGAACTGATGATTATTCAAAATAAATCCGG	3775
Qy	1221	GluIleAspPheAlaHisCysThrValLeuThrIleAlaHisIleArgLeuAsnThrIleIleAsp	1240
Db	3776	GAGAAATTTGGCCACCTGCACCGCTCTACCATTCATTCACACAGATTGAACACATTAATTGAC	3835
Qy	1241	SerAspIleValIleMetValLeuAspSerGlyArgLeuIleValGluIleProIleVal	1260
Db	3836	AGCACAAGAAAGAAATGGTTTATGATTCAGAAAGATGAAAGAAATATGATGAGCGTATGTT	3895
Qy	1261	LeuLeuGlnAsnLeuValSerLeuPheThrGlyIleMetValGlnGlnIleuGlyIleValGlu	1280
Db	3896	TTGCTCGCAAAATTAAGAGAGCTTATTTTCAAGATGTTGCACAACTGGGCGAAGCGAGAA	3955
Qy	1281	AlaAlaAlaLeuThrGluThrAlaValArgGlnValIlePheIleAsnArgAsnIleProHisIle	1300
Db	3956	GCCCTGGCCCTCAGTGAACACAGCAAAACAGGTATTACTTCAAAAGAAATTTATCCACATATT	4015
Qy	1301	GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle	1320
Db	4016	GGTCACTACTGACCAATGGTTTACAAACATTTCCATATGACAGCCCTGCACCTTACTATTT	4075
Qy	1321	PheGluThrAlaLeu 1325	
Db	4076	TTTCGAGACAGCACCTG 4090	
RESULT 11			
ADN39253			
ID	ADN39253	standard; cDNA; 4231 BP.	
AC	ADN39253;		
XX	17-JUN-2004	(first entry)	
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:571.		
XX	Human; differential expression; cancer; angiogenic disorder;		
XX	fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;		
KW	inflammatory disease; autoimmune disease;		
KW	retinal neovascularization syndrome; scarring; uterine fibroid;		
KW	detection; diagnosis; prognosis; drug screening; drug targeting;		
KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;		
XX	vulnerary; gene therapy; vaccine; gene; ss.		
OS	Homo sapiens.		
XX	WO2003042661-A2.		
PN	22-MAY-2003.		
PD			

XX 13-NOV-2002; 2002MO-US036810.
 PF 13-NOV-2001; 2001US-0350666P.
 XX 21-NOV-2001; 2001US-0332464P.
 PR 29-NOV-2001; 2001US-0334393P.
 PR 03-DEC-2001; 2001US-0335394P.
 PR 14-DEC-2001; 2001US-0340376P.
 PR 08-JAN-2002; 2002US-0347211P.
 PR 10-JAN-2002; 2002US-0347349P.
 PR 08-FEB-2002; 2002US-0355250P.
 PR 13-FEB-2002; 2002US-0356714P.
 PR 20-FEB-2002; 2002US-0359077P.
 PR 29-MAR-2002; 2002US-036809P.
 PR 04-APR-2002; 2002US-037010P.
 PR 12-APR-2002; 2002US-0372246P.
 PR 05-JUN-2002; 2002US-0386614P.
 PR 16-JUL-2002; 2002US-0396839P.
 PR 22-JUL-2002; 2002US-039775P.
 PR 22-JUL-2002; 2002US-0397845P.
 PR 09-SEP-2002; 2002US-0409450P.
 XX (BOSB-) EOS BIOTECHNOLOGY INC.
 XX Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevizi PA;
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
 XX WPI; 2003-468649/44.
 DR P-PSDB; ADN39254.
 XX Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 a nucleic acid in a biological sample.
 XX Claim 8; SEQ ID NO 571; 1385pp; English.
 XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularization syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a nucleic acid sequence of the invention.
 XX SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 4231
 Score: 6779.00 Matches: 1323
 Percent Similarity: 99.9% Conservative: 1
 Best Local Similarity: 99.8% Mismatches: 1
 Query Match: 99.9% Indels: 0
 DB: 11 Gaps: 0
 US-09-976-858-42 (1-1325) x ADN39253 (1-4231)
 QY 1 MetLeuProValTyrGlnGluValAlaLysPheProAsnProLeuGlnAspAlaAsnLeuCysSer 20
 DB 116 ATGTGCGCCCGTATCCAGAGAGGTGAAGCCCAACCGCTGCAGAGAGCCGAACATCTGCTCA 175
 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheValIleGlyHisLeuArgArgLeuGlu 40
 DB 176 CCGGAGTCTTCTTGGTGCTCAATCCCTTGTAAATGATGGCATTAAGGATTAAGG 235

QY 41 GluAspAspMetCysSerValLeuProGluAspArgSerGlnHisLeuGlyValGluLeu 60
 DB 236 GAAGATGATATGATATTCAGTCTCTCCAGAGAGCCCTCAGACGACCTTGAGAGAGATTG 295
 QY 61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysPheSerLeu 80
 DB 296 CAAAGGCTCTGGAGTAAGAAGTTTAAAGACTGAGATGAGCAGCAGAGGCTTCTTTA 355
 QY 81 ThrArgAlaIleIleLeuValCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
 DB 356 ACAAGAGCAATCAATAAGTGTACTAGCAAACTTATTTAGTTTGGGAATTTTACGTGA 415
 QY 101 IleGlnGluSerAlaValValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
 DB 416 ATTGAGAAAGGCCAAGATATCCAGCCCAATTTTGGAAAAATATATATATTTT 475
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
 DB 476 GAAATTTATGATCCCATGGAATTTGTGGCTTGAACACAGGCTACGCTATGCCAGGTTG 535
 QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
 DB 536 CTGACTTTTTCACGCTCATTTTGGCTATCTGATCATCTATATTTTATCACGCTTCAG 595
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgValAlaLeuArg 180
 DB 596 TGTGCTGGAGTATGAGTATCGAGTACCGATGCGCATATGATTTATCGAAGGACCTTGT 655
 QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
 DB 656 CTTAGTATACATGCGCATGAGGAGAACACACACAGGCCAGATATGCAATCTGCTGCAT 715
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisIlePheLeuTyrAlaGlyProLeu 220
 DB 716 GATGTGAACAAGTTTGAATCAGGTGACAGTGTCTTACCTTCCTGGGAGAGACACTGT 775
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTyrMetGluIleGlyIleSerCysLeuAlaGly 240
 DB 776 CAGGAGATCGAGTACGACCTCTCTCTGATGAGATGAGAAATATCTGCTTGTGAG 835
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuInsSerCysPheGlyLysLeuPheSerSer 260
 DB 836 ATGGAGTCTTATCATTTCTCTGCTTCTGCAAGCTTTTGGGAATTTTCTTCATCA 895
 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 DB 896 CTGAGGAGTAAACCTGCAACTTTCACGAGTCCAGAGATCAGAGCATGATGAATGAATTA 955
 QY 281 ThrGlyIleArgIleIleLeuMetCysTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
 DB 956 ACTGTATTAAGATTAATTAATATGACCTGCGGAAAAAGTATTTTCAATCTTATTAAC 1015
 QY 301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320
 DB 1016 AATTTGAGAAAGAGAGATTTCCAGATTTCTGAGAAATTTCTGCTTACGAGGAGATGAT 1075
 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
 DB 1076 TTGGCTTCTTTTTCAGTGACAGCAAAATCATCGGTTTGTGACCTTACCACTTACGCTG 1135
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyVal 360
 DB 1136 CTCTCTGCGAGTGTATCAGCCAGCCGCGTGTCTGCGAGTGAAGCTGTATGTGGGCT 1195
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
 DB 1196 GTGCGGCTGACGCTTACCTTCTTCTTCCCTCAGCAGCATGAGAGGTGTCAAGAGCATC 1255
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
 DB 1256 GTCAAGATCCGAGAGATCAGAACCTTTTGTCTACTGTATGATATCAACAGCAGCAACGCT 1315

QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
DB 1316 CAGCTGCCGTGAGATGGTAAAAAGATGGGATGGATGGACAGATTACTGCTTTTGGGAT 1375
QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGlnLeu 440
DB 1376 AAGGACATCAGAGACCCCACTACAGAGCCCTTCCCTTACGTGCAGACCTGGCAATGG 1435
QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
DB 1436 TTAGCTGTGGTGGCCCTGGAGAGAGGAAAGTCACTGTTAAAGTCCGTGCTGGG 1495
QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
DB 1496 GAATTGGCCCCCAAGTCAAGGCTGGTCAAGCTGCATGAAAGATTGCTATGTCTCAG 1555
QY 481 GlnProTrpValPheSerGlyThrLeuAspSerAsnIleLeuPheGlyValSerTyrGln 500
DB 1556 CAGCCCTGGGTGTCTCGGGAACTCGAGAGATAAATTTTATTTGGGAAAGAAATATGAA 1615
QY 501 LysGluArgTyrGlyLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
DB 1616 AAGGAACGATATGAAAAATCATTAAGCTTGTGCTGAAAAAGATTACAGCTGTGG 1675
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
DB 1676 GAGGATGGTGAATCTGATCTGATAGAGATCGGGAAACACGCTGAGTGGAGGGCAAA 1735
QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspArg 560
DB 1736 GACGGGTAAACCTTGCAAGAGCATGATCAAGATCTGACATCTATCTCTGACAGAT 1795
QY 561 ProLeuSerAlaValAspAlaGlyLysSerArgHisLeuPheGlyLeuCysIleCysGln 580
DB 1796 CCTCTCAGTGCATGATGCGGAAGTTACAGACACTTGTGCAACTGTGATTTGTGCA 1855
QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
DB 1856 ATTTTGCATGAGAAAGATCAAAATTTTATGATCACTCATGTCAGATCCCAAGGCTGCA 1915
QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlnPhe 620
DB 1916 AGTCAGATTCTGATATGAAAGATGGTAAATGGTGCAGAAAGGGCACTTACACTGATTC 1975
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnLysSerGlnGln 640
DB 1976 CTAAATCTGSTRATATTTGGCTCCCTTTTAAABAAGATATATAGAAAGTGAACA 2035
QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTyr 660
DB 2036 CCTCCAGTTCCAGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095
QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680
DB 2096 TCTCAACAATCTTACAGCTCTCTTGAAGAATGGTGTCTGTGAGAGCCAAATATACAG 2155
QY 681 AsnValProValThrLeuSerGlnGluAsnArgSerGlyLysValIleGlyPheGlnAla 700
DB 2156 AATGTCCCACTTACATCAAGAGAAACCGTTCGAAGAAAGATTGGTTTTCAGGCC 2215
QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTyrIleValPheIlePheLeuIleLeuLeu 720
DB 2216 TATTAAGAAATTAATCTCAGAGCTGGTGTCTCATGATTTCTTATTTCTCTTA 2275
QY 721 AsnThrAlaAlaGlnValAlaTyrValIleGlnAspTyrTrpLeuSerTyrTrpAlaAsn 740
DB 2276 AACACGTGAGCTTACAGGTGCTATATGTCTTCAAGATTTGGTTCATATCAGGCAAC 2335
QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyLysAsnValThrGlnLysLeuAsp 760
DB 2336 AAAACAAGATATGTAATGTCACTGTAATGAGAGGAAATATTAACCAAGAAAGTCAAT 2395
QY 761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780

DB 2396 CTTAATCTGTACTTACAGAAATTTATTCAGGTTTAACTGATGACCTTCTTTTGGCACTA 2455
QY 761 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
DB 2456 GCAGATCTCTATTTGGTATTTCTACGTCCTTGTTAATCTTCAACAACTTTCACACAGAA 2515
QY 801 MetPheGlnSerIleLeuLysAlaProValLeuPheAspArgAsnProIleGlyArg 820
DB 2516 ATGTTTGAATCAATCTGAAAGCTCCGGTATTAATCTTTGATAGAAATCCAATAGGAAGA 2575
QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
DB 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGACACTTGTGATGATTTGCTGCCGTGACGTTT 2635
QY 841 LeuAspPheIleGlnThrLeuGlnAlaValGlyAlaValSerValAlaValAlaVal 860
DB 2636 TTAGATTTCATCCAGACACTTGTACAGTGGTGGTGTGCTGTGCTGTGGTGGCCCTG 2695
QY 861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
DB 2696 ATTCCTTGATCGCAATACCTTGGTCCCTTGGAAATCATTTTCTTCTCGCGCA 2755
QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900
DB 2756 TATTTTGGAAACGTCAAGAGATGTGAAGCCCTGGATCTACAACTCGGAGTCCAGTG 2815
QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTyrThrIleArgAlaTyrLysAlaGln 920
DB 2816 TTTTCCACTGTGTATCTTCTCTCCAGGGGCTGTGACCACTCGGGCATACAAAGCAAA 2875
QY 921 GluArgCysGlnLeuLeuPheAspAlaHisGlnAspLeuHisSerGlyAlaIleTrpPheLeu 940
DB 2876 GAGAGGTCTCAGAACTGTTGATGACACACAGAAATTTACATTCAGAGGCTTGGTCTTGG 2935
QY 941 PheLeuThrThrSerArgTyrTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
DB 2936 TTTTGGACAACGTCCCGGTGGTGGCGCTGCTGATGATGATCTGTGCCATGTGTGTC 2995
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyIleValGly 980
DB 2996 ATCATCTGTGCTTTGGTCCCTGATCTTGCCAAAAATCTGAGATCCGGGCAAGTTGGT 3055
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000
DB 3056 TTGGCACTGCTCTAATGCCCTCACGCTCATGGGAGATGTTTCAAGTGTGTTCGCAAAAGT 3115
QY 1001 AlaGlyValGluAsnMetMetIleSerValGluArgValIleGlyTyrThrAspLeuGln 1020
DB 3116 GCTGAAGTTGAGAAATATGATATCTCAGTAAAGAGGATCATTTGAATACACAGACTTGA 3175
QY 1021 LysGluAlaProTrpGluTyrGlnLysArgProProAlaTyrProHisGlyGlyVal 1040
DB 3176 AAGAGAACCTTGGGAATATCAAGAAAGCCCAACACAGCTGGCCCCCAAGAGAGATG 3235
QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
DB 3236 ATAATCTTTGAACAATGTAATCTCATGTACAGTCCAGGTGGGCTCTGTACTGAAAGCAT 3295
QY 1061 LeuThrAlaLeuIleLysSerGlnLysLysValGlyIleValIleGlyArgThrGlyValAlaGly 1080
DB 3296 CTGACAGACCTCATTAATTAATCAACAGAAAGGTGGCATTTGGGAAAGAACAGACTGGA 3355
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGlnProGlnGlyLysIleTyrIle 1100
DB 3356 AAAAGTCCCTCATCTACGCCCTTTTATGATTTGTCAAGACCCGAAGATTAATTTGGATT 3415
QY 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
DB 3416 GATAAGATCTTGACAACTGAATTGAATTCACGATTTAAGGAAGAAATATGATCATATTA 3475
QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140

Db 3476 CCTCAGAACCTGTTTTCATCGTGAACAATGAGAAAACTGTGATCCCTTTAAGANG 3535
Qy 1141 HsHTRAPGLUGLLeuThraPAPAlaLeuGIngluValGInLeuValGInThrlleGlu 1160
Db 3536 CACAGAGATGAGAACTGTGATGCTTACAGAGGTACCACTTAAGAAACCAATTGA 3595
Qy 1161 AsPLeuProGlyLyMeCAsPThrGluLeuValaGluSerGlySerAsnPhseSerValGly 1180
Db 3596 GATCTTCCTGGTAAATGATCTGAATTAAGCAGATCAGATTCATTTTATGTTTGA 3655
Qy 1181 GlnArgGlnLeuValCysLeuValaArgAlaIleLeuArgGlyAsnGlnIleLeuIle 1200
Db 3656 CAAGAACAATGCTGTGCTGCTGCGGCAATTCAGGAAAAATCAGATATTTGATTAT 3715
Qy 1201 AsPGLUAThThraLaAsnValaAsPProArgThraPGLUleuIleGlnLeuValaArg 1220
Db 3716 GATGAAGGAGCGGCAAAATGTGATCCAGAACTGATGATTAATCAAAAAAATCCGG 3775
Qy 1221 GluLyPheAlaHisCysThrValLeuThrlleAlaHisArgLeuAsnThrlleAsp 1240
Db 3776 GAGAAATTTGCCCATCGACCTGCTTACATTCAGACACAGTTGAACCATTTTAC 3835
Qy 1241 SerAspLySileMeCValleuAsPserGlyArgLeuLyGluTyraSPGluProTyraVal 1260
Db 3836 AGCGACAGATTAATGTTTATGATTCAAGAAAGACTGAAGAAATATGATGAGCCGTATGT 3895
Qy 1261 LeuLeuGlnAsnLyGluSerLeuPheTyrlYsMeCValGlnGlnLeuGlyValaGlu 1280
Db 3896 TTGCTGCAAAATTAAGAGAGCTTATTTACAGAGGTGCAACAATGGGCAAGGCAAGA 3955
Qy 1281 AlaAlaAlaLeuThrGluThraLaLyGlnValTyrlPheLyArgAsnTyraProHisIle 1300
Db 3956 GCCGTGCTTCCTCAGCAAGCAACGAAACAGGATATCTTCAAAAGAAATTTTCCATAT 4015
Qy 1301 GlyHisThraPAPHisMeCValThraAsnThraSerAsnGlyGlnProSerThrlle 1320
Db 4016 GGTCACTGACCAATGATGTTTACAAACATTCATATGACAGCCCTGACCTTACTAT 4075
Qy 1321 PheGluThraPAPAlaLeu 1325
Db 4076 TTCGAGACAGCACTG 4090

RESULT 12
ACL38944
ID ACL38944 standard; cDNA; 4231 BP.
XX ACL38944;
AC 24-MAR-2005 (first entry)
DT 24-MAR-2005 (first entry)
XX
DE ABC4 coding sequence, SEQ ID 1.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX P-P8DB; ABR93962.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell

PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
PS Claim 8; SEQ ID NO 1; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is
CC the coding sequence for one such CRTP. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 4231
Score: 6779.00 Matches: 1323
Percent Similarity: 99.9% Conservative: 1
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 99.9% Indels: 0
DB: 14 Gaps: 0

US-09-976-858-42 (1-1325) x ACL38944 (1-4231)
Qy 1 MetLeuProValTyrlGlnGluValaLyPheAsnProLeuGlnAsnAlaAsnLeuCysSer 20
Db 116 ATGCTGCCCGGTACAGAGAGGTGAAGCCCAACCGCTGCGAGAGCGGAACATCGTCA 175
Qy 21 ArgValPhePheTrpTTPLeuAsnProLeuPheValIleGlyHisArgArgLeuGlu 40
Db 176 CGCGTGTCTTCGTGCTCCTCAATCCTTGTTTAAATGGCCATTAACGAGATTGAG 235
Qy 41 GluAspAspMetTyraSerValleuProGluAsPserGlnHisLeuGlyGluGluLeu 60
Db 236 GAAATGATATGATTTTCACTGCTCCAGAGACCGCTCAGACGACTTTGAGAGAGATTG 295
Qy 61 GlnGlyPheTrpAspLyGluValleuArgAlaGluAsnAspAlaGlnLyPserSerLeu 80
Db 296 CAAGGTTCTCGATTAAGAAAGTTTAAAGCTGAGATGACGACAGAAAGCTTCTTTA 355
Qy 81 ThraArgAlaIleIleLyCysTyrlTTPLySerTyrlleuValleuGlyIlePheThrlleu 100
Db 356 ACAAGAGCAATCAATTAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTAACTGA 415
Qy 101 IleGluGlnSerAlaLyValIleGlnProIlePheLeuGlyLySileAsnTyraPhe 120
Db 416 ATTGAAGAAAGTGCAGAAATGATATCAGCCATATTTTGGAAATTTTAAATTTATTTT 475
Qy 121 GluAsnTyraSPProMetAsPserValaLeuAsnThraLyraLyraAlaThraVal 140
Db 476 GAAATTTATGATCCCATGAGATTCGTGGCTTTGAACAAGGTACGCTATGACCGGTG 535
Qy 141 LeuThraPheCysThrlleuIleLeuAlaIleLeuHisIleLeuTyrlPheTyrlHisValGln 160
Db 536 CTGACTTTTTCAGCGCTCATTTTGGCTATATCTGATCATCTATATTTTATCAGTTTCA 595
Qy 161 CysAlaGlyMeCArgLeuArgValaAlaMeCysHisIleMetIleTyraArgLyraAlaLeuArg 180
Db 596 TGCTCTGGATGAGCTTACAGATGAGTACGATGCGATATGATTTTACGAAGGCACTTCGT 655
Qy 181 LeuSerAsnMetAlaMetGlyLyThrlThrlGlnIleValaLeuLeuLeuSerAsn 200
Db 656 CTTAGTAACATGGCCATGAGGGAAGACCAACCAAGCCAGATGATGCAATCTGCTGCCAAT 715

QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
Db 716 GATGTGAACAGATTGGATCATGAGGTGACAGTGTCTTATCACTTCCTGTGGGCAAGACACAGT 775
QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyIleSerCysLeuAlaGly 240
Db 776 CAGGGGATCGCAGTGCCTGCTCTGAGATGAGATGAGAAATTCGGCTTCCTGTGG 835
QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
Db 836 ATGGCAGTTCTAATCATTTCTCTGCTTGCCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 895
QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
Db 896 CTGAGAGATAAAACCTGCACTTTCACAGATGCGAGATCAGGACCATGAAATGAAATGATA 955
QY 281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
Db 956 ACTGATATAGATATATAATAATGTACCGCTGGGAAAGCTCAATTCCTATATACC 1015
QY 301 AsnLeuArgLysLeuGlnIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
Db 1016 AATTTGAGAAAGAGAGATTTCCAGATTCGAGAAATTCCTGCTCAGGGGAGATGAAAT 1075
QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
Db 1076 TTGGCTTCCTTTTTCAGTCAGCAAAATCATCGTGTGTGTGACCTTCACCACTACGCTG 1135
QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
Db 1136 CTCCTCGAGAGTGTATCAACCCAGCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1195
QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGlyArgValSerGlnAlaIle 380
Db 1196 GTGGCGCTACCGTTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1255
QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
Db 1256 GTACAGATCCGAAGATCCAGACCTTTTGTACTTGTACTGAGATATCAACGCGCAACCGT 1315
QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
Db 1316 CAGCTGCCCTCAGATGTGTAAAAAGATGTGATGTGCAGATTTTATCTCTTTTGTGGAT 1375
QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
Db 1376 AAGGATCGAGAACCCCACTTACAGGCTTTCTTACTGTCTGACCTGGCAATTTG 1435
QY 441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
Db 1436 TTAGCTGTGTGCGCCCGTGGGAGCAGGAAAGTATCATCTGTAAAGTCCGCTCGGG 1495
QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaIleTyrValSerGln 480
Db 1496 GAATTGTGCCCAAGTCAACGGCTGTGTGCAGCGTGCAGGAAGAAATTCCTATGTGTCTCG 1555
QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500
Db 1556 CAGCCCTGGGTGTCTCGGGAACCTCGAGAGTAAATTTTATTTGGGAAAGAAATATGAA 1615
QY 501 LysGluArgTyrGluLysValIleLysValAcYsValAlaLeuLysLysAspLeuGlnLeuLeu 520
Db 1616 AAGGAACGATATGAAAAAGTCAATAAGCTTGTGTCTGAAAAAAGATTACAGCTGTGG 1675
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
Db 1676 GAGGATGTGATCTGATGTATGAGATCGGGGAACCAACGCTGTGTGAGAGGCGCAAAA 1735
QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
Db 1736 GACGGGTTAACTTTCAGAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCAT 1795

QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
Db 1796 CCTCTCAGTGCAGTAGAGCCGGAAGTTAGCAGACCTGTGTGCAACTGTGTATTTGTCAA 1855
QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaIle 600
Db 1856 ATTTGCAATGAGAGATACAAATTTTACTGCTCATCTCAGTTGCGAGTACTTCAAACTGCA 1915
QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyTyrThrTrpGluPhe 620
Db 1916 AGTCAGATTCGATATTAAGATGTAAATGTGTGAGAGAGGGAAGCTTACATCAGATTC 1975
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnGlnSerGlnGln 640
Db 1976 CTAATAATCTGTATATGATTTGTGCTCCCTTTTAAAGAGATTAATGAGAAAGGAAACAA 2035
QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTrp 660
Db 2036 CCTCCAGTCCAGAGAACTCCACATAGAGATGTACCTTCTCAGAGTCTTCGGTTTGG 2095
QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGlu 680
Db 2096 TCTCAACATCTTCTAGACCTCTCTGAAATGATGTGTCTGAGAGCCAGATACAGAG 2155
QY 681 AsnValProValThrLeuSerGluGluLysAsnArgSerGlyLysValGlyPheGlnAla 700
Db 2156 AATGTCCAGTTACACTATCAGAGAGAACCGTTCTGAAAGAAAGTTGTTCAGGCC 2215
QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisArgTrpIleValPheIlePheLeuIleLeuLeu 720
Db 2216 TATAGATTTACTTCAGAGCTGTGTCTCAGATGTGTCTTCTTCTTCTTCTTCTTCTTCT 2275
QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
Db 2276 AACACTGACGTCAAGTGTCCCTATGTCTTCAAGATTTGTGTGTGTGTGTGTGTGTGTGT 2335
QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyAsnValThrGluLysLeuAsp 760
Db 2336 AAACAAAGTATGCTAAATGTCACTGTAAATGAGAGAGAAATGTAAACGAAAGCTTAAT 2395
QY 761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
Db 2396 CTTAATCTGATCTTACAGAAATTTATTCAGGTTTAACTGATGCTACCGTCTTTTGGCTA 2455
QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
Db 2456 GCAAGATCTTAATGTGATTTACGCTCTGTTAACCTTCAACAACTTGCACAAACAA 2515
QY 801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
Db 2516 ATGTTTGAATCAATTTCTGAAAGCTCCGGTATATTTCTTGTATGAAATCCAAATAGGAAGA 2575
QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
Db 2576 ATTTTAAATCGTTTCTCAAAAGACATTTGACATTTGATTTGCTCCCGCTACAGTTT 2635
QY 841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValIleSerValIleValAlaVal 860
Db 2636 TTAGATTTCAATCCAGACATTTGCTACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2695
QY 861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
Db 2696 ATTCCTGTGATCGCAATACCTTGTGTCCCTGTGAAATCAATTTTCTTCTCGGGGA 2755
QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900
Db 2756 TATTTTGGAAACCTCAAGATGTGAAGGCTCGGAATCTCAACTCGAGATCTCAATG 2815
QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
Db 2816 TTTTCCCACTTGTATCTTCTCTCCAGGGGCTGTGACATCCGGGATTAACAAAGCAGAA 2875
QY 921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeu 940

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Db      2876 GAGAGGTGCAGGAACTGTTTATGACACGAGATTTCATTCAGAGGCTTGTTCTTG 2935
Qy      941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
Db      2936 TTTTGGACACACGTCCTGGCTGTTCCGCTCCGCTCGATGATGCATCTGTCATGTTTGC 2995
Qy      961 IleIleValAlaPheGlySerLeuIleLeuAlaValThrLeuAspAlaGlyValGly 980
Db      2996 ATCATCTGCTGCTTGGGATCCCTGATCTGGCAAAACTGCGAGATCCCGGAGGTTGGT 3055
Qy      981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
Db      3056 TTGGCACTGCTCTATATCCCTCAAGCCTCATGGGAGATCTTCAGTGGTGTTCGACAAACT 3115
Qy      1001 AlaGlyValGluAsnMetCetIleSerValGluArgValIleGlnTyrThrAspLeuGlu 1020
Db      3116 GCTGAAGTTGAAATVTGATGATCTCAGTAAAGGGTCATTTGAATACACAGACCTTGAA 3175
Qy      1021 LysGluAlaProTrpGluTyrGlnLysArgProProAlaTrpProIleGlnGlyVal 1040
Db      3176 AAAGAAAGCACTTGGAAATATACAAAGACCCACACAGCCTGGCCCATAGAGAGTG 3235
Qy      1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
Db      3236 ATPATCTTTGACAAATGTGAACCTTCATGATCAGTCCAGGTGGGCTCTGTTACTGAAGCAT 3295
Qy      1061 LeuThrAlaLeuIleLysSerGlnGlyValGlyIleValGlyArgThrGlyAlaGly 1080
Db      3296 CTGACAGCACTCATTAATCACAGAAAGTTGGCATGTTGGAAAGAACCGAGCTGGA 3355
Qy      1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGlnProGlnGlyLysIleTrpIle 1100
Db      3356 AAAAGTCCCTCATCTCAGCCCTTTTATGATGTCAGAACCCGAAAGTAAATTTGGATT 3415
Qy      1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysMetSerIleIle 1120
Db      3416 GATTAAGATTTGACAACTGAATTTGACATTCACGATTTAAGAAAGAAATGTCATCATCA 3475
Qy      1121 ProGlnGluProValLeuPheThrGlyIleMetArgLysAsnLeuAspProPheAsnGlu 1140
Db      3476 CCTCAGAAACCTGTTTGTTCATCTGAAACATAGAGGAAAAACCTGGATCCCTTAAAGAG 3535
Qy      1141 HistHraPrgLugLueUtrPheAlaLeuGlnGlnValGlnLeuLysGlnThrIleGlu 1160
Db      3536 CACACGATGAGGAAGTGTGGAATGCTTACAAAGAGTACCACTTAAACCAATGAA 3595
Qy      1161 AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGly 1180
Db      3596 GATCTTCCCTGTTAAATGGAATACGAATTAAGCAATCCAGATTTTATGCTGTGA 3655
Qy      1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
Db      3656 CAAAGACAACTGGTGTGCTTCCAGAGGCAATTTCTCAGGAAATTCAGATATTATTTAT 3715
Qy      1201 AspGluAlaThrAlaAsnValAsnProAlaGlnTrpAspGlnLeuIleGlnLysValLea 1220
Db      3716 GATGAAGCGACGCAAAATGTGATCCAAAGACTGATGATTAATCAAAAAAAATCCCG 3775
Qy      1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
Db      3776 GAGAAATTTGGCCCATCGACCTGCTACCAATTGCACACAGATGAAACCACTTATGAC 3835
Qy      1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlyTyrAspGlnProTyrVal 1260
Db      3836 AGCGCAAGATATATGTTTATGATTCAGAGAACCTGAAGAAATATGATAGCGTATGTT 3895
Qy      1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
Db      3896 TTGCTGCAAAATTAAGAGAGCCATTTTACAAAGATGTCACCAACTGGGCAAGGAGAA 3955
Qy      1281 AlaAlaAlaLeuThrGlnThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300

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Db      3956 GCCGCTGCCCTCACTGAAGACAGAAACAGGATTACTTCAAAAGAAATTAATCACATATT 4015
Qy      1301 GlyHisThrAspHisMetValThrAsnThrGlnArgGlnIleProSerThrLeuThrIle 1320
Db      4016 GGTCACTGACCAATGATGTTACAAACATTCGATGACAGAGCTTCACCTTAATCTATT 4075
Qy      1321 PheGluThrAlaLeu 1325
Db      4076 TTCAGACAGCACTG 4090

RESULT 13
AEA00097
ID AEA00097 standard; cDNA; 4231 BP.
XX
AC AEA00097;
XX
DT 28-JUN-2005 (first entry)
XX
DE Human TAT131 cDNA SEQ ID NO:49.
XX
KW ss; gene; tumor-associated antigen; cytostatic; breast tumor;
KW endocrine disease; gynecology and obstetrics; neoplasm; colon tumor;
KW gastrointestinal disease; rectal tumor; endometroid carcinoma;
KW genitourinary disease; renal tumor; lung tumor; respiratory disease;
KW ovary tumor; skin tumor; liver tumor.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 116..4093
FT CDS /tag= a
FT /product= "TAT131"
FT
XX
PN US2005106644-A1.
XX
PD 19-MAY-2005.
XX
PP 08-SEP-2004; 2004US-00936626.
XX
PR 20-JUN-2001; 2001US-0299500P.
PR 29-JUN-2001; 2001US-030180P.
PR 18-SEP-2001; 2001US-0323268P.
PR 19-JUN-2002; 2002US-0017748P.
PR 26-MAR-2004; 2004US-0557115P.
PR 04-AUG-2004; 2004US-0596899P.
XX
PA (GENTH ) GENENTECH INC.
XX
PI Caltns B, Chen R, Frantz G, Hillan KJ, Koepfen H, Phillips HS;
PI Polakie P, Spencer SD, Smith V, Williams PM, Wu TD, Zhang Z;
PI Sliakowski M;
XX
DR WPI; 2005-384304/39.
DR P-PSDB; AEA00175.
XX
PT Novel isolated antibody capable of binding to tumor-associated antigenic
PT target polypeptide, useful for treating cell proliferative disorder e.g.
PT cancer.
XX
PS Claim 1; SEQ ID NO 49; 337pp; English.
XX
CC The invention relates to a novel isolated antibody binding to a
CC polypeptide having at least 80% sequence identity to a polypeptide having
CC any one of 76 fully defined 182-910 amino acid tumor-associated antigenic
CC target polypeptide (TAT) sequences (AEA00127-AEA00202) given in the
CC specification, a polypeptide having any one of (AEA00127-AEA00202),
CC lacking its associated signal peptide, or an extracellular domain of a
CC polypeptide having any one of (AEA00127-AEA00202). The polypeptide is
CC encoded by the nucleotide sequence having any one of (AEA0049-AEA00126).
CC An antibody of the invention has cytostatic activity. The antibody is
CC useful for inhibiting growth of a cell expressing TAT188, which involves
CC contacting the cell with the antibody. The cell is a cancer cell chosen
CC from breast, colon, rectum, endometrium, kidney, lung, ovary, skin and

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CC liver cell. The cancer cell is a mammalian cell, preferably a human cell.
 CC The antibody is also useful for detecting the level of TAT188
 CC polypeptide expressed in a test cell relative to a control cell, and for
 CC detecting the level of TAT188 polypeptide or a polypeptide having at
 CC least 80 % sequence identity to the TAT188 polypeptide sequence in a test
 CC cell relative to a control cell. The antibody is useful for treating a
 CC preventing a cell proliferative disorder associated with increased
 CC expression or activity of a polypeptide having at least 80 % identity to
 CC a TAT188 polypeptide sequence. The cell proliferative disorder is cancer.
 CC The method of the invention is useful for inhibiting the growth of a
 CC cancer cell. The present sequence encodes a polypeptide of the invention.

XX Sequence 4231 BP, 1170 A, 895 C, 1015 G, 1151 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4231
Score:	6779.00	Matches:	1323
Percent Similarity:	99.9%	Conservative:	1
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	99.9%	Indels:	0
DB:	14	Gaps:	0

US-09-976-858-42 (1-1325) x AEA00097 (1-4231)

QY 1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCySer 20
 DB 116 ATGCTCCCGTGTACAGAGAGGTGAAGCCCAACCCGCTGACGAGACGCAATCTGCTCA 175
 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
 DB 176 CCGGTTCTTCTGGGCTCAATCCCTGTTTAAATGGCCATTAACGGAGATTAGAG 235
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlnGluLeu 60
 DB 236 GAAAGATGATGATGATTCAGTGTCCGCAAGACCGCTCAACAGCCTTGGAAGAGAGTTG 295
 QY 61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
 DB 296 CAAGGTTCTGGGATTAAGAAGTTTAAAGCTGAAGATGACGACAGAAAGCCTTCTTTA 355
 QY 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyLysPheThrLeu 100
 DB 356 ACAAGACATCATTAAGTTGTTACGGAATCTTATTAGTTTGGAAATTTTTCAGTTA 415
 QY 101 IleGlnGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
 DB 416 ATTTGAGGAAGTCCCAAGTAATCCAGCCCATTTTTTGGAAAAATTTTAAATTTATTTT 475
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140
 DB 476 GAAATTTATGATCCCATGATCTGTGGCTTGAACACAGCCGTACCCCTATGCCACGGTG 535
 QY 141 LeuThrPheCysThrIleuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
 DB 536 CTGACTTTTGGACCGCTCATTTTGGCTATATCTGCATCACTTAAATTTTATACAGTTG 595
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
 DB 596 TGTGCTGGATGAGGTTCAGAGTACGCAATGTGCCATATGATTTATTCGAAAGCACTTCGT 655
 QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlnIleValAsnLeuLeuSerAsn 200
 DB 656 CTTAGTAACATGGCCCATGGGGAAGACACACAGGCCAGATAGTCAATCTGCTGTCCAT 715
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
 DB 716 GATGGAAACAAGTTTATCATGAGTGACAGAGTCTTACCTTCTGTGGCAGACACCACTG 775
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTyrMetGlnIleGlyLysSerCysLeuAlaGly 240
 DB 776 CAGGCATGCACTGACCTGCTACTCTGTGATGAGATAGAAATATCGTGGCTTGTGGG 835
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260

DB 836 ATGGAGTTCTTAATCATCTCTGCTGCAAGCGTCTTTGGAACTTTCTTCACACA 895
 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 DB 896 CTGAGATTAATACTGCAACTTTTACGGAATCCAGATTCAGACCATTAAGAACTTATA 955
 QY 281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGlyLysSerPheSerAsnLeuIleThr 300
 DB 956 ACTGGTATTAAGATATATAAATGTAACCGCTGGGAAAGTATTTTCAAACTTATTTACC 1015
 QY 301 AsnLeuArgLysGlnIleSerLysIleLeuArgSerSerCysLeuArgIleMetAsn 320
 DB 1016 AATTGAGAAAGAAAGAAATTTCCAAAGTTCTGAGAAAGTTCTGCTTACAGGGGATGAA 1075
 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrTyrVal 340
 DB 1076 TTGGCTTGTTTTCAGTGCAGCAAAATCATCGTTTGGACCTTACCACTACCTACG 1135
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
 DB 1136 CTCCCTCGCAGTGTGATCAGACCGCAGCGGTGTTCTGGCAGTGAACCTGTATGGGGCT 1195
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
 DB 1196 GTGCGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGTTCTCAGAGCAATC 1255
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuAspGluIleSerGlnArgAsnArg 400
 DB 1256 GTACAGATCCAGAAATCAGAACCTTTTGTCTACTTGAATGAGATTCACAGCCAGCCGT 1315
 QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
 DB 1316 CAGTCCCGTCAGATGTAAAGATGGTGCATGACAGATTTTACCTTTTGGGAT 1375
 QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
 DB 1376 AAGGATCAGAGACCCCAACTCTACMAAGCCTTTCTTACTGTGACGCTGGCGAAATG 1435
 QY 441 LeuAlaValAlaGlyProValAlaValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
 DB 1436 TTAGCTGTGTGCGGCCCTGGAGACAGGAAGTACATCACTTTAAGTCGCTGCGGG 1495
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
 DB 1496 GAATTGGCCCAAGTCAAGGCTGGTCAAGCATGGAAGAAATGCTATGTGCTCAG 1555
 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
 DB 1556 CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAAATATTTATTTGGGAAAGAAATATGAA 1615
 QY 501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 DB 1616 AAGGACATATGAAAAAGTCAATAAGCTTGTGCTCGAAAAAGATTTTACAGCTGTG 1675
 QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
 DB 1676 GAGGATGATGATCTGACTGTGATAGAGATCGGGGAACACAGCTGAGAGGGGAGAAA 1735
 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
 DB 1736 GCACGGGTAAACCTTGGCAAGAGCAAGTGTATCAAGATGCTGACATCTACTCTCGACCAT 1795
 QY 561 ProLeuSerAlaValAspAlaGlyValSerArgHisLeuPheGluLeuCysIleCysGln 580
 DB 1796 CCTCTCAGTGAAGATGAGAGGAGTGAAGACACCTTGTTCGAACTGTGATTTTGTCAA 1855
 QY 581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
 DB 1856 ATTTTGCATGAGAAATCAACAATTTTATGATCACTAGTGTGACGTACTCAAGCTCA 1915
 QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620

Db 1916 AGTCAGATTCTGATATTGAAAGTGGTAAATGCTGCAGAGGGACTTACAGTAGTTTC 1975
 Qy 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
 Db 1976 CTAAATATCGGATATGATTTGGCTCCCTTTAAAGAAAGATATACAGAAAGTGAACA 2035
 Qy 641 ProProValProGlyThrProThrLeuAArgAsnArgThrPheSerGluSerSerValTyr 660
 Db 2036 CTTCCAGTTCCAGAAATCCCACTACAGAAATCGTACCTTCTCAGAGCTTCCTGGTTGG 2095
 Qy 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680
 Db 2096 TCTCAACATCTTTCAGACCTCTCTGAAAGATGGTCTCTGAGAGCCAAAGTACAGAG 2155
 Qy 681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
 Db 2156 AATGTCGCCAGTACCTATCAAGAGAGAAACCGTTCGAAAGAAAGTTGGTTTCAGGCC 2215
 Qy 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTyrPheIleValPheIlePheLeuIleLeuLeu 720
 Db 2216 TATTAAGATTACTTCAGAGCTGGTGTCTCACTGGATTGTTCTTCAATTTCTTATTTCTCTA 2275
 Qy 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrTrpLeuSerTyrTrpAlaAsn 740
 Db 2276 AACACTGCAGCTCAGGTTGCTATGTCCTTCAAGATTGGTGGCTTTCATCTGGGCAAC 2335
 Qy 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyAsnValThrGluLysLeuAsp 760
 Db 2336 AAACAAGATCTAAATGTCACCTGAAATGAGAGGAAATGTAAACCAAGAACAGTAGAT 2395
 Qy 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
 Db 2396 CTTAACTGGTACTTACGAAATTTATTCAGGTTTAACTGATGCTACCGTTCCTTTTGGCATA 2455
 Qy 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
 Db 2456 GCAAGTCTCTATGGTATTTCTACGTCCTGTGTTAACTCTTCAAACTTGGCACAACAA 2515
 Qy 801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
 Db 2516 AAGTTTGAATCAATCTGAAAGCTCCGGTATTAATCTTGTATGAAATCAATAGACAA 2575
 Qy 821 IleLeuAsnArgPheSerLysAspIleGlyHisIleAspAspLeuLeuProLeuThrPhe 840
 Db 2576 ATTTTAAATCGTTTCTCCAAAGCATTTGACACTTGGATGATTGTGTGCGCTGACGTT 2635
 Qy 841 LeuAspPheIleGlnThrLeuLeuGlnValAlaGlyValIleSerValAlaValAlaVal 860
 Db 2636 TTAAATTTCAATCAAGACATTTGCTACAGTGGTGTGGTGTCTCTGTGGCTGTGGCCGTG 2695
 Qy 861 IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
 Db 2696 ATTTCTTGGATCGCAATACCTTGGTCCCTTGGATCATTTTCTTCTGGCGCA 2755
 Qy 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
 Db 2756 TATTTTGGAAACGTCAGAAATGAAAGCGCTGGAAATTCACAACTGGAGTCCAGAG 2815
 Qy 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTyrThrIleArgAlaTyrLysAlaGlu 920
 Db 2816 TTTTCCCATTTGTCAATCTTCTCTCCAGGGGCTCTGGACATCCGGGCAACAAAGAGAA 2875
 Qy 921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeu 940
 Db 2876 GAGAGGTGCAGAAATGTTTGAATGACACCAAGATTTACATTCAGAGGCTTGGTCTTG 2935
 Qy 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
 Db 2936 TTTTGGACAAAGCTCCGCTGGTTCGCGCTCCGCTGGATGCCATTCGTCCCAAGTTTGTG 2995
 Qy 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
 Db 2996 ATCATGCTGTCCTTGGGTCCCTGATTTGGCAAAATCTGTGATGCCGGGCAAGTTGGT 3055

Qy 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000
 Db 3056 TTGGCAGTCTCCTAATGCTCTCAAGCTCATGGGGAATGTTTCAGTGGTGTTCACAAAGT 3115
 Qy 1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGln 1020
 Db 3116 GCTGAAGTTGGAATATATATATATCTCAATGAAGGCTCATTTGAATACAGACCTTGA 3175
 Qy 1021 LysGluAlaProTyrGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
 Db 3176 AAAGAAGCAGCTTGGGAATATCAGAAACCCACCAAGCTGGCCCCCATGAAGAGAG 3235
 Qy 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
 Db 3236 ATAACTTTGACAAATGTAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3295
 Qy 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
 Db 3296 CTGACAGCATCTAATTAATTCAGAAAGAGTTGGCATTTGGGAAAGAACCGGAGCTGGA 3355
 Qy 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
 Db 3356 AAAAGTCCCTCATCTCAGCCCTTTTATGATTGTCAAGAACCCGAAGTAAATTTGGATT 3415
 Qy 1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
 Db 3416 GATTAAGATCTTGACAACTGAATGTGAATGTGACTTCAAGATTTAAGAAAGAAATGTCAATCATA 3475
 Qy 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
 Db 3476 CCTCAGAAACCTGTTTGTTCATCTGACATGAAACATAGGAAGAAACCTGGATCCCTTAAAGAG 3535
 Qy 1141 HisThrAspGluGlnLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
 Db 3536 CACAGGATGAGAACTGTGAAATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3595
 Qy 1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
 Db 3596 GATCTTCTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 3655
 Qy 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
 Db 3656 CAAGACAACTGTGTGCTGCTGCCAGGGCAATTCACAGAAATTAACATATTTGATTAT 3715
 Qy 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
 Db 3716 GATGAAGGAGCGGCAAAATGTGATTCAGAACTGATGATTAAATCAAAAAAATCCGG 3775
 Qy 1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleLeuP 1240
 Db 3776 GAGAAATTTGGCCATCTGACCGGTGTAACTATGACACAGATTTAAACCACTTATTTGAC 3835
 Qy 1241 SerAspLysIleMetValLeuAspSerGlyLysArgLeuLysGluTyrAspGluProTyrVal 1260
 Db 3836 AGCGCAAGATATATGTTTATGATTACAGAAAGCTGAAGAAATATGATGAGCCGATGTT 3895
 Qy 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
 Db 3896 TTGCTGCAAAATTAAGAGAGCTTATTTTACAAAGATGGTGAACCAACTGGGCAAGCAADA 3955
 Qy 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
 Db 3956 GCCGTGCTCTCAGAAACAGCAAAACAGGATATCTTCAAAAGAAATTAATTCACATATT 4015
 Qy 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
 Db 4016 GGTCACTGACCAATGATTAACAAACATCTTCAATGACAGCCCTGACCTTAATCTATT 4075
 Qy 1321 PheGluThrAlaLeu 1325
 Db 4076 TTGAGAGACAGCACTG 4090

RESULT 14
 ID AEA00617 strand: cDNA; 4231 BP.
 AC AEA00617;
 DT 28-JUL-2005 (first entry)
 DE Human TAT131 cDNA sequence SeqID49.
 XX
 KM antibody identification; tumor-associated antigen; cytostatic;
 KM RNA interference; gene therapy; cell death; cancer; breast tumor;
 KM colon tumor; rectal tumor; renal tumor; lung tumor; ovary tumor;
 KM skin tumor; liver tumor; gene; ss; TAT131.
 XX
 OS Homo sapiens.
 PN US2005107595-A1.
 PD 19-MAY-2005.
 PF 10-SEP-2004; 2004US-00938061.
 XX
 PR 20-JUN-2001; 2001US-0299500P.
 PR 29-JUN-2001; 2001US-0301880P.
 PR 18-SEP-2001; 2001US-0323268P.
 PR 19-JUN-2002; 2002US-00177488.
 PR 26-MAR-2004; 2004US-0557116P.
 PR 04-AUG-2004; 2004US-0598899P.
 XX
 PA (GENTH) GENENTECH INC.
 PI Cairns B, Chen R, Frantz G, Hillan KJ, Koepfen H, Phillips HS;
 PI Polakis P, Spencer SD, Smith V, Williams PM, Wu TD, Zhang Z;
 PI Sakanaka C, Chundharapai A, Reed CJ;
 DR WPI; 2005-371577/38.
 DR P-PSDB; AEA00695.
 XX
 PT Novel isolated antibody e.g. anti-R16 or anti-TAT131 antibody that binds
 PT to tumor-associated antigenic target polypeptide, useful for diagnosing
 PT or treating cancer.
 XX
 PS Claim 1; SEQ ID NO 49; 96pp; English.
 XX
 CC This invention relates to a novel isolated antibody, for example anti-R16
 CC or anti-TAT131 antibody, that binds to a tumor-associated antigenic
 CC target polypeptide (TAT) and that lacks an associated signal peptide
 CC sequence. The invention may be useful for the development of compounds
 CC with a cytostatic activity acting as antagonists of the TAT188
 CC polypeptide or RNA interference whilst the disclosed sequences may be
 CC useful for gene therapy. The invention is useful for inducing the death
 CC of a cell (such as a cancer cell chosen from breast, colon, rectum,
 CC endometrium, kidney, lung, ovary, skin and liver) to which it binds,
 CC inhibiting proliferation or promoting cell death of a cell expressing
 CC TAT188. In addition, the invention may be useful for detecting the level
 CC of TAT188 polypeptide in a test cell relative to a control cell, or
 CC treating or preventing a cell proliferative disorder associated with
 CC increased expression of TAT188. The novel antibody of the invention is
 CC useful for inhibiting the growth of a cancer cell and may be useful for
 CC diagnosing or treating cancer. The present sequence is that of the human
 CC TAT131 cDNA which encodes a protein against which an antibody of the
 CC invention may be targeted.
 XX
 SO Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 4231
 Score: 6779.00 Matches: 1323
 Percent Similarity: 99.9% Conservative: 1
 Best Local Similarity: 99.8% Mismatches: 1
 Query Match: 99.9% Indels: 0
 DB: 14 Gaps: 0

US-09-976-858-42 (1-1325) x AEA00617 (1-4231)
 QY 1 MetLeuProValIYrGlnGluValIlyrProAsnProLeuGlnAspAlaAsnLeuCySer 20
 Db 116 ATGCTGCCGCGTACAGAGAGTGAAGCCCGCTGCAGAGCCGAACATCTGCTCA 175
 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheUyllegYHslYsArgArgLeuGlu 40
 Db 176 CGCGTGTTCTTGTGTGCTCAATCCCTGTTTAAATTTGGCCATPAACGAGATTAG 235
 QY 41 GluAspAspMetYrSerValLeuProGluAspArgSerGlnHslLeuGlyGlnGluLeu 60
 Db 236 GAAAGATGATATGATATTCAGTGTCCAGAAAGCCGCTCAGACACCTTGAGAGAGTTG 295
 QY 61 GlnGlyPheTrpAspLyGluValLeuArgAlaGluAspAlaGlnLyPheSerLeu 80
 Db 296 CAAGGATTCGTGGATTAAGAAAGTTTAAAGCTGAAGATGACGACAGAGCTTCTTA 355
 QY 81 ThrArgAlaIleIleIleYsCySerYrTrpLySerYrLeuValLeuGlyIlePheThrLeu 100
 Db 356 ACPAAGACATCATPAAGTGTACTGAAATCTTATTTAGTTTGGAAATTTTTCGTTA 415
 QY 101 IlegIuGluSerAlaIyValIlegIuProIlePheLeuGlyIleIleAsnYrPhe 120
 Db 416 ATTGAGAAAGTGCMAAGTATCCAGCCCATTTTGGAAAAATTTATTAATTTT 475
 QY 121 GluAsnYrAspProMetAspSerValAlaLeuAsnThrAlaYrAlaYrAlaThrVal 140
 Db 476 GAAATTTATGATCCCATGATTTCTGTGCTTGAACACAGCGTACGCTATGCCGAGT 535
 QY 141 LeuThrPheCyStrLeuIleLeuAlaIleLeuHslHslsLeuYrPheYrHslValGln 160
 Db 536 CTGACTTTTGGACCGCTCATTTTGGCTATACGATCACTTAATTTTATCAGCTT 595
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHslsMetIleYrArgLyAlaLeuArg 180
 Db 596 TGTGCTGGATGAGGTTCAGGTACGATGCGCATGATGATTTATCGAAGGACCTTGT 655
 QY 181 LeuSerAsnMetAlaMetGlyLyStrThrThrThrGlyGlnIleValAsnLeuSerAsn 200
 Db 656 CTTATGATACATGCGCATGGGAAAGCAACACAGGCCAGATGATCATCTGTGTCAT 715
 QY 201 AspValaLeuLyPheAspGlnValThrValPheLeuHslsPheLeuTrpAlaGlyProLeu 220
 Db 716 GATGTGAACAAGTTTGATCAGGTGACAGGTCTTACACTTCTGTGGGACGACACTG 775
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIlegYHslsCysLeuAlaGly 240
 Db 776 CAGGGGATCGCAGTACCTGCTCTGAGATGAGATGAAATTCGCTTGTGCG 835
 QY 241 MetAlaValIleIleIleLeuLeuProLeuGlnSerCysPheGlyLyLeuPheSerSer 260
 Db 836 ATGGCAATTCATATCATTTCTCTGCCCTTGCAAACTGTTTGGAAAGTGTTCATCA 895
 QY 261 LeuArgSerLyStrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 Db 896 CTGAGAGATTAACCTGCAACTTTCACGATGCCAGATCAGACCATGATGAATATA 955
 QY 281 ThrGlyIleArgIleIleIleYsMetYrAlaTrpGluYrSerPheSerAsnLeuLeuThr 300
 Db 956 ACTGTATTAAGATATATAAATGTACCGCTGGGAAAGTCATTTTCAATTTATTC 1015
 QY 301 AsnLeuArgLyLeuGluIleSerYsIleLeuArgSerCysLeuArgLyMetAsn 320
 Db 1016 AATTGAGAAAGAAAGAGATTTTCAAGATTCGAAAGTTCTGCTCAGGGGAGTAAAT 1075
 QY 321 LeuAlaSerPhePheSerAlaSerLyIleIleValAlaPheValThrPheThrThrYrVal 340
 Db 1076 TTGGCTGTGTTTTCAGTGCAGCAAAATCATCGTGTGACCTTCCACCTACGCG 1135
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuYrGlyVal 360

Db	1136	CTCTCCGGCAGGTGATATCAGACCGCCGGTTCGTGGCAGTACCGCTGTATGGGCT	1129
QY	361	ValAArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle	380
Db	1196	GTCGGCGCTGACGGTTACCTCTTCTCCCTCAGCCATTGAGAGGGGTGTCAAGAGCAATC	1255
QY	391	ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAspArg	400
Db	1256	GTCACATATCCGAAGATCCAGACCTTTTGTCTACTGTATGATGATATATCAGACGCAACGT	1315
QY	401	GlnLeuProSerAspGlyIleIysMetValHisValGlnAspPheThrAlaPheTrpAsp	420
Db	1316	CAGCTGCCGTGACAGATGCTAAAAAGTGTGCATGTGCAGGATTTTACTGCTTTTGGGAT	1375
QY	421	LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu	440
Db	1376	AAGGATCAGAGACCCCAACTCTACAGAGCCTTTCTTACTGTACAGCTGGGGAATGT	1435
QY	441	LeuAlaValAlaGlyProValGlyAlaGlyIysSerSerLeuLeuSerAlaValLeuGly	460
Db	1436	TTAGCTGTGTCTGGCCCGGTGGAGCAGAGAACTCATCTGTTAAAGTCCGTCTCCGG	1495
QY	461	GluLeuAlaProSerHisGlyLeuValSerAlaHisGlyArgGluAlaTyThrValSerGln	480
Db	1496	GAATTGGCCCCAAGTACACGGGGTGTACGGCTGACGTGAGAAATTTGCTTATGTCTCAG	1555
QY	481	GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyIleArgTyrcIu	500
Db	1556	CAGCCCTGGGTGTCTTCGGGAACCTGTAGAGATATATTTRTTTGGGAAGAAATATGAA	1615
QY	501	LysGluArgTyrcIuIysValIleIysAlaCysAlaLeuIlyAspLeuGlnLeuLeu	520
Db	1616	AAGGAACATATGAAAAAGTCAAAAGCTTGCTGTGAAAAAGATTTTACACTGTGTG	1675
QY	521	GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnIys	540
Db	1676	GAGGATGGTGTACTGACTGTATAGAGATCGGGACACCGCTGAGTGGAGGGCAGAAA	1735
QY	541	AlaArgValAsnLeuAlaArgAlaValTyrcIuAspAlaAspIleTyrcLeuLeuAspAsp	560
Db	1736	GCACGGCTAAACCTTGCAAGAGCACTGTATCAAGATGTGACATCTACTCTGACGAT	1795
QY	561	ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln	580
Db	1796	CCTCTCAGTGCAGTGTATGCGGAAGTGTAGCAGACACTTGTTCGAACGTGTATTGTCAA	1855
QY	581	IleLeuHisGluIysIleThrIleLeuValThrHisGlnLeuGlnTyrcLeuIysAlaAla	600
Db	1856	ATTTTGTCAGGAAMATCACAATTTTATGTACTCATCGTTGCAGTACCTCAAGCTGCA	1915
QY	601	SerGlnIleLeuIleLeuIysAspGlyIysMetValGlnIysGlyThrTyrcThrGluPhe	620
Db	1916	AGTCAGATTTCGATTGTAAAGATGTAAAAATGGTGCAGAAAGGGGACTTACACTGAGTTC	1975
QY	621	LeuIysSerGlyIleAspPheGlySerLeuLeuIysIlyAspAsnGluGlnSerGluGln	640
Db	1976	CTAAATCTGGATATGATTTTGGCTCCCTTTTAAAGAGGATTAATAGAGAAAGTGAACA	2035
QY	641	ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp	660
Db	2036	CCTCCAGATCCAGGAACCTCCACACTAAGGATCTTACTCTCAGATCTTCGGTTTGG	2095
QY	661	SerGlnIysSerSerArgProSerLeuIysAspGlyAlaGlnGluSerGlnAspThrGlu	680
Db	2096	TCTCAACATCTTCTAGACCTCTCTTGAAGATGTGTCTGAGAGGCAAGATACAGAG	2155
QY	681	AsnValProValThrLeuSerGluGluAsnArgSerGluGlyIysValGlyPheGlnAla	700
Db	2156	AATGTCCCAAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAAGTTTCAGGCC	2215
QY	701	TyrcIysAsnTyrcPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu	720
Db	2216	TATAAAGATTTACTCAGAGCTGTGTCTCACTGAGATTTGCTTCAATTTCTTAATCTCTTA	2275

QY	721	AsnThrAlaAlaGlnValAlaIleTyrValLeuGlnAspTyrProPheSerTyrTrpAlaAsn	740
Db	2276	AAACATGAGCTCAGGTGGCTTAATGCTTCAAGATGGTGGCTTCACTACGGGGCAAC	2333
QY	741	LygGlnSerMetLeuAsnValThrValAsnGlyGlyAsnValThrGlyLeuLeuAsp	760
Db	2336	AAACAAATATGATCTAAATGCTCACTGTAAATGAGAGGAAATGTATACCGAAGACTGAT	2399
QY	761	LeuAsnTyrPyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle	780
Db	2396	CTTAACCTGTCCTTAGGAATTTATTCAGAGTTAACTGTAGCTACCGTCTTTTGGCATTA	2455
QY	781	AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys	800
Db	2456	GCAAGATCTTATTTGGTATTTCTTAGCTCTTGTAACTTTCACAAACTTTGGACAAACA	2515
QY	801	MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg	820
Db	2516	ATGTTTAGTCAATTCTGAAGCTCCGGTATTTATTTCTTGATAGAAATCCAAATAGAGA	2573
QY	821	IleLeuAsnArgPheSerSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe	840
Db	2576	ATTTTAAATCTTTTCTCCAAAGACATTTGACACTGTGATGATTTGCTCCCTGACGTTT	2633
QY	841	LeuAspPheIleGlnThrLeuLeuGlnValGlyValValSerValAlaValAlaVal	860
Db	2636	TTAGATTTCACTCAACACATCTGCTACAGTGGTGGTGGTGGTCTCTGTGGCTGTGGCCTG	2693
QY	861	IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg	880
Db	2696	ATTCCTTGATCGCAATACCTCTGGTTCCTCTGGAAATCAATTTTCATTTTCTTCGGGGA	2753
QY	881	TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal	900
Db	2756	TATTTTTCGAAACGTCAGAGAGTGTAAAGCCCTGGAAATCTTCAACTCGAGTCCAGTG	2815
QY	901	PheSerHisLeuSerSerSerSerLeuGlnGlyLeuTyrThrIleArgAlaTyrLysAlaGlu	920
Db	2816	TTTTCCCACTGTCACTTTCTCTCCAGGGGCTGTGACATCCGGGCAATACAAAGACAA	2875
QY	921	GluArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTyrPheLeu	940
Db	2876	GAGAGGTGTCAAGAACTGTGTGATGACACACAGATTTTCAATTCAGAGGCTTGGTCTTG	2933
QY	941	PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal	960
Db	2936	TTTTTGACAAAGTCCCGCTGGTGTGGCCTCCGTCTGATGCACTGTGGCATGTTTGTCT	2993
QY	961	IleIleValAlaPheGlySerLeuIleLeuAlaYsThrLeuAspAlaGlyGlnValGly	980
Db	2996	ATCATCGTTGGCTTTGGGTGCCCTGATTTGGCAAAAATCTGTGATCCGGGACAGGTGGT	3053
QY	981	LeuAlaLeuSerTyrAlaAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer	1000
Db	3056	TTGGACATGCTCTATGCCCTCAACGCTCAATGGGAAAGTTCACAGGTGGTGTGACAAAGT	3115
QY	1001	AlaGluValGluAsnMetMetIleSerValGluArgValIleGlyTyrThrAspLeuGlu	1020
Db	3116	GCTGAAGTTGAATATGATGATGATGATGCAATGAAGGGTCATTGAATACACAGACTTGAA	3175
QY	1021	LysGluAlaIleProTyrGlyTyrGlnLysArgProProAlaTyrProHisGlyGlyVal	1040
Db	3176	AAAGAAAGCACTTGGGAATATCAAGAAAGCCACACACAGCTGGCCCCCAAGAAAGAGTGG	3233
QY	1041	IleIlePheAspAsnValAsnAspMetTyrSerProGlyGlyProLeuValLeuLysHis	1060
Db	3236	ATTAATCTTGACATATGATCACTTCAATGACAGTCCAGGTGGGCTCTGTGATCTAAGCAT	3293
QY	1061	LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValAlaGlyArgThrGlyValGly	1080
Db	3296	CTGACAGCACTCAATTAATCAACAAGAAAGGTTGGCATTTGGGAGAGAACCGGAGCTCGGA	3355

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QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGluValysIleTrrpIle 1100
DB 3356 AAAAGTTCCCTCATCTCAGCCCTTTTATGATTTGTGAGAACCCGAAAGTAAATTTGGANT 3415
QY 1101 AspIysIleLeuThrGluIleGluLeuHsAspLeuArgLysMetSerIleIle 1120
DB 3416 GATAGATCTGACAACTGAAATTTGACTTCACGATTTTAAAGAGAAATGCAATCAATA 3475
QY 1121 ProGlnGluProValLeuPheThrGluThrMetArgLysAsnLeuAspProPheAsnGlu 1140
DB 3476 CCTCGAGAACTGTTGTTTGTCTGACGAAACATGAGAAACCTGGATCCCTTTAAGAG 3535
QY 1141 HisTrpAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
DB 3536 CACACGAGATGAGAACTGTGGAATGCTTACAAAGAGTCAACTTAAAGAAACCAATTGA 3595
QY 1161 AspLeuProGluLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
DB 3596 GATCTTCCCTGTTAAATGATGATCTGAAATTAAGCAGATCCCAATTTTGTGTGGA 3655
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
DB 3656 CAAAGCAACTGCTGTGCTTCCGAGGCAATTTCTCAGAAATCAAGATTTGATTATT 3715
QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
DB 3716 GATGAAGCAGCGCAATGTGGATCCAAAGACTGATGATTAATCAAAAAAATCCGG 3775
QY 1221 GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
DB 3776 GAGAAATTTGCCACGACCGCTGCTAACCATTTGCAACAGATTTGAAACCACTTTATGAC 3835
QY 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
DB 3836 AGCGACAAATTAATGTTTAAATTCAGAAAGCAAGCAAAATATATATGACCCGATGTT 3895
QY 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGluLysAlaGlu 1280
DB 3896 TTGCTGCAAAATTAAGAGAGCCCTATTATTCAGAGATGTGTCAACCACTGGGCAAGCAGAA 3955
QY 1281 AlaAlaIleLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
DB 3956 GCGCGTCCCTCACTGAAACAGCAAAACAGGATATCTTCAAAAGAAATTAATCCACATATT 4015
QY 1301 GlyHisThrAspHisMetValThrAsnTrpSerAsnGlyGlnProSerThrLeuThrIle 1320
DB 4016 GGTCACTGACCACTGCTTCAAACTTCATCAATGACAGCCCTCGACTTAATCTATT 4075
QY 1321 PheGluThrAlaLeu 1325
DB 4076 TTCAGACAGCACTG 4090

```

RESULT 15

ADR66822
ID ADR66822 standard; DNA; 5832 BP.

AC ADR66822;

DT 02-DEC-2004 (first entry)

DE Human prostatic carcinoma derived DNA SEQ ID 115 #4.

XX human; cytostatic; diagnosis; prostatic cancer;

KW differential expression analysis; ds.

OS Homo sapiens.

PN WO2004076614-A2.

PD 10-SBP-2004.

PF 22-FEB-2004; 2004WO-DE000433.

PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILAR/) PILARSKY C.
XX
PI Hinmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T,
PI Schmitt A, Beckmann G, Bruemendorf T, Kimmernann H, Roepcke S,
PI Kinzhong L, Staud E;
XX
PS WPI, 2004-653386/63.

PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.

Claim 1; Page 1348-1349; 1607pp; German.

This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumor cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CC CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The CC samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and CC lymph node metastases were also stained. ADR65805-ADR65954 represent the CC polynucleotide and polypeptide sequences used in the method of the invention.

SEQ Sequence 5832 BP; 1660 A; 1175 C; 1306 G; 1691 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	5832
Score:	6779.00	Matches:	1323
Percent Similarity:	99.9%	Conservative:	1
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	99.9%	Indels:	0
DB:	13	Gaps:	0

US-09-976-858-42 (1-1325) x ADR66822 (1-5832)

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QY 1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaLeuCysSer 20
DB 116 ATGCTGCCCTGTATCAGAGAGGTGAAGCCCAACCCGCTGACGAGACGCAATCTGCTCA 175
QY 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGluHisLysArgLysGlu 40
DB 176 CGCGTGTCTTCTGTGCTGCTCAATCCCTTTAAATTTGGCAAAACGAGATTAGG 235
QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGluGluLeu 60

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Db 226 GAAAGATGATATGATATTCAGTGTCCAGAAAGCCGCTCAGACACTTGGAAGAGAGTTG 295
 Qy 61 GINGIYPHEPTRAPSLYGLIValleuargalaglueasaplaaglulysproserleu 80
 Db 296 CAAGGGTTCGGAGTAAAGAGTTTAAAGAGCTGAGAAAGACGACAGAAAGGCTTCCTTAA 355
 Qy 81 ThrAGAlaIleIleleCyseTyrTrpLysSerTyrLeuValleuGlyIlePheThrleu 100
 Db 356 ACAAGGACATCATTAAGTGTATCTGAAATCTTATTTAGTTTGGAAATTTTACGTTA 415
 Qy 101 IlegluguserAlalyValIlegIlePheleuGlyLysIleleasnyrPhe 120
 Db 416 ATTGAGAAAGTGCCAAAGTAAATCCAGCCCATATTTTGGAAATATTAATTAATTTT 475
 Qy 121 GIUAenTYrAspProMetCaspSerValAlaleuAsenThrAlaTYrAlaThrVal 140
 Db 476 GAAAAATTATGATCCCATGGAATTCGTGCTTGGAACACAGCGTACGCCCTATCCACGGTG 535
 Qy 141 LeuThrPheCyseThrleuIleleuAlaIleleuHISleLeuTYrPheTYrHISValGln 160
 Db 536 CTGACTTTTGCACGCTCATTTTGGCTATCTGACATCACTTATATTTTATCACTTCAG 595
 Qy 161 CybalagIlyMeCArgLeuArgValAlaMeCysHISMeCileTYrArgLysAlaLeuArg 180
 Db 596 TGTGCTGGGATGAGGTACGAGTAGACATGTGCCATATGATTTATCGGAAGGCACTTCGT 655
 Qy 181 LeuSerAsenMetAlaMeCglyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
 Db 656 CTTACTTAACNTGGCCATGGGGAAGACACACAGGCCAGATAGTCAATCTGCTGCTCAT 715
 Qy 201 AspValAsnLysPheAspGlnValThrValPheLeuHISpHeLeuThrAlaGlyProleu 220
 Db 716 GATGGAACAAATTTGATGAGGTGACAGTGTCTTACACTTCTGCGGACAGACACACG 775
 Qy 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyIleSerCysLeuAlaGly 240
 Db 776 CAGGAGATCGAGTAGTGCCTCACTCGGATGAGATGAGAAATCGGCTTCGCTGG 835
 Qy 241 MetAlaValleuIleIleleuLeuProleuGlnSerCysPheGlyLysLeuPheSerSer 260
 Db 836 ATGGCAGTTCATATCTCTCTGCTTCGACAAAGCTGTTTGGGAAGTGTTCATCACTCA 895
 Qy 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 Db 896 CTGAGAGATTAACCTGCACTTTCACGAGTGCAGAGATCAGAACATGATTAAGTATA 955
 Qy 281 ThrGlyIleArgIleIleLysMetTYrAlaTrpGlyLysSerPheSerAsnLeuIleThr 300
 Db 956 ACTGCTATTAAGATTAATAAATGTAACGCTCGGAAAGTCAATTTTCAAACTTATTAAC 1015
 Qy 301 AsnLeuArgLysLeuGlnIleSerLysIleleuArgSerSerCysLeuArgIlyMeCAsn 320
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 Qy 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTYrVal 340
 Db 1076 TTGGCTGTGTTTTCAGTGCAAGCAAAATCATCGTGTGTAACCTTCAACCTCAACG 1135
 Qy 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTYrGlyAla 360
 Db 1136 CTCCTCGGAGGTGATCAACAGCCGCGCTTCGTGCGAGTACACGCTGATGGGGCT 1195
 Qy 361 ValAlaGlyLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGlnAlaIle 380
 Db 1196 GTGCGCGTGAACGGTTACCTCTTCTTCCCTCAGCATTAAGAGGGGTGCAAGCAATC 1255
 Qy 381 ValSerIleArgArgIleGlnThrPheLeuLeuAspGlnIleSerGlnArgAsnArg 400
 Db 1256 GTACACATCCGAAGAAATCCAGACCTTTTGTACTTGATGAGATATCAAGGGCAACGCT 1315
 Qy 401 GlnLeuProSerAspGlyLysLysMetValHISValGlnAspPheThrAlaPheTrpAsp 420

Db 1316 CAGTCGCGTCAAGTGTAAAGATGTGATGTGACAGATTTTACTGCTTTTGGAT 1375
 Qy 421 LysAlaSerGlnThrProThrleuGlnIleLysSerPheThrValArgProGlyGlnLeu 440
 Db 1376 AAGGATCAGAGAACCCCAACTCTTACAGGCCCTTCTTACTGTGACAGCTGGCAATTG 1435
 Qy 441 LeuAlaValAlaGlyProValGlyValaGlyLysSerSerLeuLeuSerAlaValleuGly 460
 Db 1436 TTAGCTGTGTGCGCCCGTGGAGACAGAGAGTATCATCTTTAAAGTCCGCTCGCG 1495
 Qy 461 GIUeulAlaProSerHISGlyLeuValSerValHISGlyArgIleAlaTYrValSerGln 480
 Db 1496 GAATTGGCCCCAAGACAGGGCTGGTCAGCGTGACGTGAGAAATGCTTATGTCTCAG 1555
 Qy 481 GlnProTrpValPheSerGlyTYrThrLeuArgSerAsnIleleuPheGlyLysLysTYrGln 500
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 Qy 501 LysGluArgTYrGlyLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 Db 1616 AAGGACATATGAAAAAGTCAATAAGCTTGTCTGAAAAGAAATTTACAGCTGTG 1675
 Qy 521 GIUAepGlyAspLeuThrValIleGlyAspArgGlyTYrThrLeuSerGlyGlyGlnLys 540
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 DB 2516 AGTTTGAAGTCAATTCGAAAGCTCCGGATTAATCTTTGATGAAATCCAAATAGAAAGA 2575
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 DB 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGAGACACTTGGATGATTTGTGCGCGTGCAGTTT 2635
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 QY 861 IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
 DB 2696 ATTTCTTGGATGCAATACCCCTTGGTCCCTTGGATCATTTTTCATTTTCTTGGCGCA 2755
 QY 881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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 DB 4076 TTCGAGACAGCACCTG 4090

Search completed: March 14, 2006, 08:36:53
 Job time : 1773 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2006, 08:37:01 ; Search time 1315 Seconds
(without alignments)
5478.823 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6787

Sequence: 1 MLPVQEVKPNPLQDANLCS.....WVTNTSNGQPSLTITFETAL 1325

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abbs/ABSSWEB_spool/US09976858/runat_13032006_170101_11806/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=ab8808
-USER=US09976858 @CCN_1_1_5315 @runat_13032006_170101_11806 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*
1: gb_esc1.*
2: gb_esc2.*
3: gb_esc3.*
4: gb_hic.*
5: gb_esc4.*
6: gb_esc5.*
7: gb_esc6.*
8: gb_esc7.*
9: gb_gse1.*
10: gb_gse2.*
11: gb_gse3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5864	86.4	4594	4	AK0522778 Mus muscu
2	5553	81.8	3685	10	AY415506 Homo sapi
3	4828	71.1	3679	10	AY415508 Mus muscu
4	4395	64.8	3685	10	AY415507 Pan trogl
5	2582	38.0	3208	4	AK032802 Mus muscu
6	2263	33.3	5920	4	AK029876 Mus muscu
7	2216.5	32.7	5899	4	CR749835 Homo sapi

8	2144	31.6	4547	4	BC046560 Mus muscu
9	2138	31.5	4953	10	CL969772 OsRIFCC018
10	2046.5	30.2	4638	11	DQ044660 Homo sapi
11	2043.5	30.1	4080	11	DQ038460 Homo sapi
12	1968.5	29.0	4185	10	AY407265 Homo sapi
13	1957.5	28.8	4176	10	AY407267 Mus muscu
14	1955	28.8	4483	10	CL957124 OsRIFCC019
15	1942.5	28.6	4425	10	CL970490 OsRIFCC019
16	1920.5	28.3	4185	10	AY407266 Homo sapi
17	1888.5	27.8	4452	10	CL968077 OsRIFCC016
18	1883	27.7	4224	11	DQ049053 Homo sapi
19	1880	27.7	4425	10	CL963465 OsRIFCC009
20	1861	27.4	4773	11	DQ045352 Homo sapi
21	1835.5	27.0	1655	4	CNS0668R
22	1822.5	26.9	4080	11	DQ038461 Homo sapi
23	1817	26.8	4161	10	CL952237 OsRIFCC013
24	1813.5	26.7	3561	10	CL966129 OsRIFCC013
25	1797	26.5	4443	10	AY399795 Homo sapi
26	1784.5	26.3	4686	10	CL969658 OsRIFCC018
27	1781	26.2	4149	11	DQ038456 Homo sapi
28	1726	25.4	4542	10	AY412332 Homo sapi
29	1706.5	25.1	3588	10	CL964834 OsRIFCC011
30	1697	25.0	4529	10	AY412334 Mus muscu
31	1688	24.9	3975	10	AY399797 Mus muscu
32	1682.5	24.8	4638	11	DQ044661 Homo sapi
33	1661.5	24.5	1493	4	CNS0FQBA
34	1657	24.4	3561	10	CL979509 OsRIFCC033
35	1624	23.9	3597	10	CL966131 OsRIFCC013
36	1536	22.6	2516	4	AK049174 Mus muscu
37	1520	22.4	4773	11	DQ045353 Homo sapi
38	1514.5	22.3	2397	10	CL958547 OsRIFCC001
39	1507	22.2	4905	10	CL963549 OsRIFCC009
40	1501	22.1	3361	4	AK083916 Mus muscu
41	1499.5	22.1	3174	11	DQ050048 Homo sapi
42	1455	21.4	4242	4	AY399796 Homo sapi
43	1317	19.4	1195	8	DN698293 ClJ16-G03
44	1250.5	18.4	4460	11	DQ030756 Homo sapi
45	1250	18.4	1084	3	BM462073 AGENCOURT

ALIGNMENTS

RESULT 1	AK0522778	4594 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK0522778				
DEFINITION	Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, Clone:Db30049P08 product:ATP-binding cassette, gub-family C (CFTR/MRP), member 4 homolog (Human), full insert sequence.				
ACCESSION	AK0522778.1 GI:26095372				
VERSION	HTC, CAP trapper.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 Carninci, P. and Hayashizaki, Y.				
AUTHORS	High-efficiency full-length cDNA cloning				
TITLE	Meth. Enzymol. 303, 19-44 (1999)				
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
AUTHORS	Genome Res. 10 (10), 1617-1630 (2000)				
TITLE	11042159				
REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M., Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K.,				

TITLE
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
PUBMED
11076861

REFERENCE
AUTHORS
4

TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
REFERENCE
AUTHORS
5

TITLE
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS
6

TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

JOURNAL
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
1. 4594

FEATURES
source
1. 4594

misc_feature
1. 4594

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 4594
Score: 5864.00 Matches: 1131
Percent Similarity: 92.5% Conservative: 74
Best Local Similarity: 86.9% Mismatches: 96
Query Match: 86.4% Indels: 1
DB: 4 Gaps: 0

US-09-976-858-42 (1-1325) x AK052778 (1-4594)

QY 25 TTTTTPLeuAaPProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMet 44
DB 166 TGGTGGCTCAACCGCGCTTTAAAACTGGTCATAAAGCGAGACTGGAAGAGACATGACATG 225
QY 45 TyrsValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheThr 64
DB 226 TTTCAAGCTTCCAGAAAGATCGCTCAAGAGACCTCGAGAGAGACTTCAACGGATGAC 285
QY 65 AspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIle 84
DB 286 GATTAAGAACTTTCGACAGCCAAAGAGACTCGAGAGAGCCCTCTTAAAGGACATC 345
QY 85 IleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGlnSer 104
DB 346 ATAAAGTGTACTGGAAGTCTTACCTGATTTTGGGAAATTTTACGTTAATTAGAGAGAGGC 405
QY 105 AlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAsp 124
DB 406 ACTGAGTAAATTCAGCCCTTATTTTACGGGAAATTAATTAATTTTGAAGATATGAC 465
QY 125 ProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCys 144
DB 466 CCCGACGACTGGTGGCTTTCGATACAGCTTATGCTTACGAGAGAGCTGCTCATGTC 525
QY 145 ThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGlnCysAlaGlyMet 164
DB 526 ACGCTCATCTGGCCATCTACTCATCATATTGTACTTGTACACAGTCGAGTCGCGCGGATG 585
QY 165 ArgLeuAlaGluValAlaMetCysHisMetLeuTyrArgLysValAlaLysLeuSerAsnMet 184
DB 586 AGGCTGCGGTTGCGCAGTGTGCACATGATTAACGGAGAGGACCTCGGTTAAGTAACTCG 645
QY 185 AlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLys 204
DB 646 GCCATGGGAAAGACACACAGCCAGATATTAACTGCTGTCACAGAGTGAACAA 705
QY 205 PheAspGlnValThrValPheLeuHisPheLeuTyrAlaGlyProLeuGlnAlaIleAla 224
DB 706 TTCGACCAAGACATCTTCTGCACTTCTGTCGAGGCGGCTGCAACCCATCGC 765
QY 225 ValThrAlaLeuLeuTyrMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeu 244
DB 766 GTAACCGTCTCTCTGGTGAGATAGAAATCTCTGCGGAGGCTGTCGCTG 825
QY 245 IleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLys 264
DB 826 GTATTCTTCTGCTCTGCAAGCTCATCGGAAAGCTTCTGCTCATCTCGGAGTAA 885
QY 265 ThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArg 284
DB 886 ACTGGGCTTTCAGGAGTCCAGAGTCCGAGCATGAATGAATGATTAACAGGATGAGG 945
QY 285 IleIleLysMetTyrAlaTyrGluLysSerPheSerAsnLeuIleThrAsnLeuArgLys 304
DB 946 ATAAATAAAGATGATGCTGGAGAAATCGTTTGCTGACCTCATTCGCCAAATCTTAAGAAAG 1005
QY 305 LysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhe 324
DB 1006 AAGGAGATTTCCAGATTTCTGGCGAGCTCTCACTCAAGAGGATGAACATGGCTGTTT 1065
QY 325 PheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySer 344
DB 1066 TTCATCGCAACCAAGTCATCTGTCGTCGTCATCTCACTCACTGCTGTCGTCAT 1125
QY 345 ValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyValAlaValArgLeuThr 364
DB 1126 GAGATTACAGGTAGCAAGTGTGTGGCCATGACTGTGACGGTCCGTTGGTGCA 1185
QY 365 ValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArg 384
DB 1186 GTACACCTCTTCTTCCGTCGACCATTTGAGAGAGGCTCAAGGCCATGTCATGCACTTCG 1245

QY 385 ArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSer 404
 Db 1246 AGGATCAAGAACTTCTTCTACTGATGATACACAGCGCAAGCCCATGTACATCT 1305
 QY 405 AspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGlu 424
 Db 1306 GATGGCAAGCAATGTCTCAAGTCGACAGATTTCACCGCTTCTGGGACAGGCACTAGAC 1365
 QY 425 ThrProThrLeuGlnGlyLeuSerPheThrValAspProGlyGluLeuLeuAlaVal 444
 Db 1366 AGTCACACCTCGCAAGGCTCTTCTTATTCGACAGCGCTGGAGATTGTTCAGCCCTGGTT 1425
 QY 445 GlyProValGlyAlaGlyLysSerSerLeuSerAlaValLeuGlyGluLeuAlaPro 464
 Db 1426 GGGCCAGTTGGAGCGCAAGTCGTGCTTGGACGAGCTGCTGGAGAGCTGCTCTCT 1485
 QY 465 SerHisGlyLeuValSerValHisGlyArgIleAlaIleAlaIleSerGlnGlnProTrpVal 484
 Db 1486 GCCAGCGGGCTGTGACGGGTGACGGGAGATCGCTACGTTTCTCACAGCCCTGGGTG 1545
 QY 485 PheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysGlyLysGlyLysArgTyr 504
 Db 1546 TTCTCGGGCACCGTGAGAGCAATATTTATTTGGAAAGAAATATGAGAGAGGAGATAT 1605
 QY 505 GluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuGluAspGlyAsp 524
 Db 1606 GAGAAAGATGATCAAGGCTGTGCTGTGAAGAGACCTGCACTTCTGAGAGACGGGAT 1665
 QY 525 LeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsn 544
 Db 1666 CTGACGGTTATAGAGACCGGGAGACCAAGCTGATGAGAGGCAAGAGCTGGGTGAC 1725
 QY 545 LeuAlaAlaGlyAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAla 564
 Db 1726 CTGGACCGGGCGCTGTACAGAGCCGCAATCTACCTCTTGAGATCGGCTGACCGCT 1785
 QY 565 ValAspAlaGlyValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGln 584
 Db 1786 GTTCATGCGAAGTGGGCAAGACCTGTTCACACTGTGTATCTGTACAGCGCTTGACAG 1845
 QY 585 LysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeu 604
 Db 1846 AAGATCACCATTTTATGTGATCAGCAAGTTTACAGTCTCAAGGTCGACAGCACTCTC 1905
 QY 605 IleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGly 624
 Db 1906 ATACTCAAGATGTGTGAGATGTGTGCAAGAGGGGCACTTACACGAGTTTCTGAAATCTGT 1965
 QY 625 IleAspPheGlySerLeuLeuLysLysAspAsnGlyLysGlnProProValPro 644
 Db 1966 GTAGATTTTGGCTCCCTGTTAAAGAAAGAAAGCAAGAGAGAGCCCTCCACAGCCCA 2025
 QY 645 GlyThrProThrLeuArgAsnArgThrPheSerGlyLysSerValTyrPheSerGlnLysSer 664
 Db 2026 GGAACCCCGACACTCAGGAAAGCAACTTCTCCGAGGCTCAATTGGTCTCAGAGTCA 2085
 QY 665 SerArgProSerLeuLysAspGlyAlaLeuGlyLysGlnAspThrGluAsnValProVal 684
 Db 2086 TCCAGACCTCGTGTAAAGACGGGGCCCGACAGGCGCAAGAGAGAGAGCAAGAGCA 2145
 QY 685 ThrLeuSerGlyLysAspArgSerGlyLysValGlyPheGlnAlaTyrTyrAsnTyr 704
 Db 2146 GTGCAACCCGAGAGAGCGGTCGGAAGGAGAGATCGGCTTCAAGGCTCAAGAAATTAC 2205
 QY 705 PheArgAlaGlyAlaHisIleTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAla 724
 Db 2206 TTCTGGGGGGGGGACCTCGGTTTCATCATTTTCTTGTGCTCTTAACTAGTGGGCT 2265
 QY 725 GlnValAlaIleTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMet 744
 Db 2266 CAGGTTTCTATGTTCTTCAAGACTGTGGCTTTCCTCCAGTGGCGCAAGCAAGAGTGTCA 2325
 QY 745 LeuAsnValThrValAsnGlyGlyGlyLysAsnValThrGluLysLeuAspLeuAsnTrpTyr 764

Db 2226 CTGAACAACACAGAAATGCGAATGTAAATATACGAGAGACCTTAGACCTGAGCTGGTAC 2385
 QY 765 LeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeu 784
 Db 2386 TTAGAAATTTTACGAGGTCTTAACTGCGGTACCTCTCTTTTGGCATAGCAAGATCTCTTA 2445
 QY 785 LeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGlySer 804
 Db 2446 CTGGGTCTATATCTTGTGAACGCTTCCAGACTTTCACACAGAGATTGTGAGTTC 2505
 QY 805 IleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArg 824
 Db 2506 ATACTGAAGGCTCCCGTGTGTTCTTTCGACAGAAATCAATCGGAGAGATTTTAATGCT 2565
 QY 825 PheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIle 844
 Db 2566 TTCTCCAAAGACATCGGACATCATGATGATTGCTTCCCTGAGCGTCTCGACTTCATC 2625
 QY 845 GlnThrLeuLeuGlnValGlyValValSerValAlaValAlaValIleProTrpIle 864
 Db 2626 CAGAGTGTCTCTCGTGTAGTGTATGCTGTGGCCGCGCGCTGATCTTGGATTC 2685
 QY 865 AlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGlu 884
 Db 2686 CTCAATACATTTGTTCCGCTCTCAGTGTCTTCTCTGTTCTTGGAGATCTTCTAGAG 2745
 QY 885 ThrSerArgAspValLysValGlyLeuGlyLysThrThrArgSerProValPheSerHisLeu 904
 Db 2746 ACGTACGGGATGTCAAGCGCTGGAATCCCAACAGAGAGCCGGAATTTCTCCATTTA 2805
 QY 905 SerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysValGlyGluArgCysGln 924
 Db 2806 TCGTCTCTCCACAGGACTGTGACCAATCCGGGCTTACAAAGCTGAGAGAGGTGTGAG 2865
 QY 925 GluLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeuPheLeuThrThr 944
 Db 2866 GAGCTGTTTATGACACACAGAGCTTGCATTCAAGGCTTGTCTTCTGTCGACGACA 2925
 QY 945 SerArgTrp-PheAlaValArgLeuAspAlaIleCysAlaMetCysValIleIleValAla 964
 Db 2926 TCGAGATGTTTCCCTGTGCGCTGACGCGCATCTGGCGCATCTTGTGAATCGTGTGC 2985
 QY 964 aPheGlySerLeuLeuLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSer 984
 Db 2986 CTTCGGGCTCTTGTTCGTGGAGAACTTGAATGTGGGAGGTGGCTGGGCTGTGC 3045
 QY 984 TTYrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGlyValAla 1004
 Db 3046 CTACGCCCTCACACTCATGGGAGATGTTCCAGTGTCTGTGACAGAGCCGCAAGTGA 3105
 QY 1004 uAsnMetIleSerValGlyArgValIleGlyTyrThrAspLeuGlyLysGlyAlaPro 1024
 Db 3106 GAATATGATGATTTCACTGAGAGAGATGATGATTAACGAGCTAGAGAGAGAGGCC 3165
 QY 1024 CTGTGlyTyrGlnLysArgProProProAlaTrpProHisGlnGlyValIleIlePheAs 1044
 Db 3166 TTGGAGAGCAAGAGGCGCCACCCAGGCTGGCCCGACAGAGAGATCATGTCTTGA 3225
 QY 1044 PAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisIleLeuThrAla 1064
 Db 3226 CATGTGAATCTTCACTACAGCTTACAGCTTACAGTGGGCTCTGTGTTTGAAGACCTGAGCT 3285
 QY 3286 CATCAAGCTCAGGAAAGAGTTGGATTTGGGCAAGAACCGGAGCTGGGAAATCTCCCT 3345
 QY 1084 uIleSerAlaLeuPheArgLeuSerGlyProGlyGlyLysIleTrpIleAspLysIleLe 1104
 Db 3346 CATCTGGGCTCTTCAAGCTGTGAGAACCCGAGAGGAGAAATCTGGATCATAGATCTT 3405
 QY 1104 uThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnLysPro 1124

Db	3406	GACAAACCAAAATGGGCTTACGACTTAAGAAAGAAAATGTCATCATACCAACAGAAACC	3465
Qy	1124	oValleuPheThrglyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspG1	1144
Db	3466	TGTTTCTTCACTGACACCAATGAGAAAACCTGAGCCCTTCAATGACACAGGACGA	3525
Qy	1144	uGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProG1	1164
Db	3526	GGAGCTGTGAGAGGCTTGGAGAGGATCAACTTAAGAGGCACTTGAAGATCTTCGG	3585
Qy	1164	LYLeuMetAspThrglyLeuLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgG1Le	1184
Db	3586	AAAAATGATGATCGAATTAGAGAACTGGAATCTGGAATTCAGTTGTCAGACAGACAGT	3645
Qy	1184	uValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleLeuAspGluAlaTh	1204
Db	3646	AGTGTGCTTCTGACAGGCGCATTTCTAAAGATTAACGATATCTGATCTTGAAGACAAAC	3705
Qy	1204	rAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAl	1224
Db	3706	TGCAATGTGACCCAGAACGATGAGTTAATACAGAGATCCGGAGAAAGTTTGC	3765
Qy	1224	aHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleLeuAspSerAspLysG1I	1244
Db	3766	CCAGTGCACAGTCTCACCATTGCTCACAGACTGAAACCATCATTTGACAGTGAAGAT	3825
Qy	1244	eMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAs	1264
Db	3826	AATGTTTTGATTCAGAAAGCTGAAGAAATATATGAGCCGTATGCTTCTGTCAGAA	3885
Qy	1264	nLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaIleAlaLe	1284
Db	3886	TCCAGAGAGCCCTTTTACAAAGATGTTTCAGCACTGGGCAAGGCGCAAGCCGCTCCCT	3945
Qy	1284	uThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIleGlyHisThrAs	1304
Db	3946	CACCAAAACAGAAAACAGTATCTTCAGACGGAATTAACCACTATTACATTACACAG	4005
Qy	1304	pHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAl	1324
Db	4006	CCCCCGGTTATGAACACTCTCCATGAGACGCCCTCGGCTTTAACAAATTTTGAACAGC	4065
Qy	1324	aleu 1325	
Db	4066	ATTG 4069	
RESULT 2			
LOCUS	AY415506	3685 bp	DNA linear
DEFINITION	Homo sapiens ABC4 gene, VIRUAL TRANSCRIPT, partial sequence,		GSS 17-DEC-2003
ACCESSION	AY415506		
VERSION	AY415506.1	GI:39771465	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 3685)		
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civeallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science	302 (5652), 1960-1963	(2003)
REFERENCE	2 (bases 1 to 3685)		
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejaritwal, A., Todd, M.A., Tanenbaum, D.M., Civeallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.		

TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..3685		
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>3685 /gene="ABCC4" /locus_tag="HCM5580"		
ORIGIN			
Alignment Scores:			
Pred. No.:	0		
Score:	5553.00		
Percent Similarity:	90.1%		
Best Local Similarity:	90.1%		
Query Match:	81.8%		
DB:	10		
US-09-976-858-42 (1-1325) x AY415506 (1-3685)			
Qy	63	PheTTPAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArg	82
Db	2	TTCTGGGATTAAGAAGTTTAAAGCTGAGATGACGACAGAAAGCTTTTAAACAAGA	61
Qy	83	AlaIleIleLysCysTyrTTPLysSerTyrLeuValLeuGlyIlePheThrLeuIleGlu	102
Db	62	GCAATCATTAAGTGTTCATGGAATCTTATTTAGTTTGGAAATTTTACCTTAATTGAG	121
Qy	103	GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsn	122
Db	122	NNNNNTGCCAAGTATATCCATATTTTGGGAAATTAATTAATTAATTTTGAAT	181
Qy	123	TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr	142
Db	182	TATGATCCCATGATGATTTGCTGGCTTGAACACAGCGTACGCTTATGCCAGCTGCTACT	241
Qy	143	PheCysThrLeuIleLeuAlaIleLeuHisHisIleuTyrPheTyrHisValGlnCysAla	162
Db	242	TTTTCACAGCTCATTTTGGCTATACATCATCTTATTTTATACGTTTCAGTGTGCT	301
Qy	163	GlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSer	182
Db	302	GGATGAGGTTTACAGTACGATGCGCATGTGATTTATCGGAAGNNNNNNNNNNNNNN	361
Qy	183	AsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspVal	202
Db	362	NN	421
Qy	203	AsnLysPheAspGlnValThrValPheLeuHisPheLeuTPAlaGlyProLeuGlnAla	222
Db	422	NN	481
Qy	223	IleAlaValThrAlaLeuLeuThrMetGluIleGlyIleSerCysLeuAlaGlyMetAla	242
Db	482	ATTGCAAGTACCTGCCCTTCTCTGATGAGATGAGAAATATGCTGCTTGGGATGCA	541
Qy	243	ValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArg	262
Db	542	GTTTCAATCATTTCTCCCTGCTGCAAGCGTTTGGGAAGTTGTTCTCATCACTGAGG	601
Qy	263	SerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGlnValIleThrGly	282
Db	602	AGTAAACCTGCAACTTTACCGATGCCAGATCCAGATCCAGATGAAGATTATTAATCTG	661
Qy	283	IleArgIleIleLysMetTyrAlaTTPGluLysSerPheSerAsnLeuIleThrAsnLeu	302
Db	662	ATTAAGATTAATTAATTAATGAGCTGGGAAAGTCAATTTTCAATTTTACCAATTG	721

OY	303	ArglyslvsgluileSerlyslleleuAagserSerCyLeuAarglylmetanleuA	322
Db	722	AGAAAGAAAGAAATTTCCAGAAATTCAGAAAGATTCCTGCTCAGAGGGATGAATTTGGCT	781
OY	323	SerPhePheSerAlaSerlysllelleValPheValThrPheThrThyTrValleuLeu	342
Db	782	TCATTTTTCAGTGCAGCAAGCAAAATCATCGTGTGTGTGACCTTCAACCACTACGTGCTCTCC	841
OY	343	GlySerValIleThrAlaSerAargValPheValAlaValThrLeuTyrglyValAlaArg	362
Db	842	GGCAATGTGATCAACAGCCAGCCGGCGTTCGTGGCAGTGAACCTGATAGGGCTGCGCG	901
OY	363	LeuThrValThrLeuPhePheProSerAlaleGluAargValSerGluAlaIleValSer	382
Db	902	CTGACGGTTACCTCTCTTCTTCCCTCAGCAATGGAGGGTGTCAAGAGCAATCGTCAGC	961
OY	383	IleAArgIleGlnThrPheLeuLeuAaPgluileSerGlyAargAaArgIleuLeu	402
Db	962	ATCCGAAGATCCAGACCTTTTGTGCTACTTGATGAGATTTCAAGCGCAACCGTCAAGCTG	1022
OY	403	ProSerAaPglYlyslYsMetValIslaValGlnAaPheThrAlaPheTrpAaPylsAla	422
Db	1022	CCGTCAAGATGGTAAAAAGATGTGATGTGCAAGATTTTACGCTTTTGGATGAAGCA	1081
OY	423	SerGluThrProThrLeuGlnGlyLeuSerPheThrValAaPProGlyGluLeuAla	442
Db	1082	TCAGAGACCCCAACTTCAAGAGCCCTTCTTACTGTCAAGACCTGGCCGAATTTGTAGCT	1141
OY	443	ValValGlyProValGlyAlaGlylysSerSerLeuSerAlaValleuIlyGluLeu	462
Db	1142	GTGTCGGCCCGTGGAGACAGAGAAATCATCATCTGTAAAGTCGGTGTCCGGAGAAATGG	1201
OY	463	AlaProSerHleGlyLeuValSerValHleGlyAargIleAlaTyrrValSerGlnIlePro	482
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OY	503	ArgTyrglylyslValIlelyslAlaCysAlaLeuLylyslAaPgluLeuLeuGluAaP	522
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OY	523	GlyAaPleuThrValIleGlyAaPArgGlyThrThrLeuSerGlyGlyGluTyrsAlaArg	542
Db	1382	GGTATCTGACGTGTATGAGAGATCGCGGGAACCAAGCTGAGTGGAGGCGCAAGAACACGG	1441
OY	543	ValAaLeuAlaAaArgAlaValTyrglnAaPAlaAaPleTyrrLeuLeuAaPProLeu	562
Db	1442	GTAACCTTGCAGAGACAGTGTATCAAGATGCTGACATCTATCTCTGGACGATCCTCTC	1501
OY	563	SerAlaValAaPAlaGluValSerArgHlsleuPheGluLeuCyallleGleGlnIleleu	582
Db	1502	AGTGAGATGAGTCCGAAAGTTAGCAGACACTTGTTCGAACGTGTGATTTGTCAAAATTTTG	1561
OY	583	HleGlylyslleThrIleleuValThrHleGlnleuGlnTyrrLeuTyrsAlaAlaSerGln	602
Db	1562	CATGGAAGATCAACAATTTAGTACTCATCAAGTTCAGTACTCAAAAGCTGCAAGTCAAG	1622
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Db	1622	ATTCTGATATTCGAAGATGTGTAATATGGTGCAGAGGGGACTTACATCGAGTTCTTAA	1681
OY	623	SerGlyIleAaPhePheGlySerleuLeuLylyslAaPheGlnGluSerGluIleProPro	642
Db	1682	TCTGTATATGATTTTGGCTCCCTTTTAAAGAAAGATATGAGAAAGAGCAACCTCCA	1741
OY	643	ValPProGlyThrProThrLeuAargAaArgThrPheSerGlySerSerValTyrrSerGln	662
Db	1742	GTTCCAGGAATCCCAACAATAAGAAATGTCACTTCTCAAGATCTTGGTGTGGTCTCAA	1801
OY	663	GlnSerSerAaPProSerleuLylyslAlaLeuGlnSerGlnAaPThrGlnAaVal	682

Db	1802	CAATCTTAAACCTCTCTTAAAGATGTCCTCGAGACC	CAGATACAGAGATGTC	1861
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Db	1862	CCAAGTTACACTACATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAAGCCCTATAG		1922
Qy	703	AsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnTrp		722
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Qy	723	AlaIaGlnValAlaIleValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnIleGln		742
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Qy	743	SerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluValLeuAspLeuAsn		762
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Qy	823	AsnArgPheSerIleAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAsp		842
Db	2282	AATCGTTTCTCCAAAGACATTGGACACTTGATGATTTGGCGCGCTGACGTTTAAAT		2341
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Qy	923	CysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeu		942
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 REFERENCE 1 (bases 1 to 3679)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.O.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL gene trions
 Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 3679)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.O.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
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Db	3535	NN	3594
Qy	1262	uGluAsnYsgluSerleuPheYrYlyMetValGluGluLeuGlyYsAlaGluAlaAl	1282
Db	3595	GCAGATCCAGAGACCTCTTTACAAATGTGTTCAGCACTGGGCAAGGGCGAAGCGCG	3654
Qy	1282	aAlaLeuthrGluThrAlaYsgln	1290
Db	3655	TGCCCTCACAGAAACGAAACAG	3679
RESULT 4			
AY415507			
LOCUS	AY415507	3685 bp	DNA linear GSS 17-DEC-2003
DEFINITION	Pan troglodytes ABC4 gene, VIRUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY415507		
VERSION	AY415507.1 GI:39771466		
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

[illegible]

Db 2642 ACAAGCTCCGCTGCTGCTGCTGCTGATGCCATCTGTCATGTTGTCATCATC 2701
 Oy 963 VALAAlapheglSerleuileleualalystrleuaspalagllylnvalygleuala 982
 Db 2702 GTTGCTTTGGGCTCCCTGATTTGCGAATAAACTCTGGATGCCGGGAGGTTGGTGGCA 2761
 Oy 983 leuSerTyralleuThreuleuMetglMetPheglntTpxCyvalargGlnserAlaglu 1002
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 Oy 1003 VALGluaspMetMetleleSerValgluargVallelgluTThrasplendulysglu 1022
 Db 2822 GTTGGAAATATATATATCTCAGTAGAAAGGTCATTGAATACACAGACTTAAAAAGGA 2881
 Oy 1023 AlapTpxgluTyrglnlysaRppPropoalTpxProHlsglnlyVallelle 1042
 Db 2882 GCACTTGGGAATATCAGAAAGCCACACCGGCTGGCCCCATGAGAGATGATATATC 2941
 Oy 1043 PheaspasnValasnPheMetTySerProglyglProleuValleulysHlsleuThr 1062
 Db 2942 TTTGCAATGATGAATTCATGTACAGTCCAGGTGGGCTCTGTACTGAAAGCATCTGACA 3001
 Oy 1063 AlaleuIllelySerGlnlyllyValylylleValyArgThrglylaGlyllysser 1082
 Db 3002 GCACTCATTAATCAACANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3061
 Oy 1083 SerleuileSerAlaleuPheargleuSerGluProgluGlylyleTllepIleasplys 1102
 Db 3062 NNN 3121
 Oy 1103 lleleuThrThrgluIlleglyleuHlsaspleuArglyllyMetSerlleleProglu 1122
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 Oy 1123 GluProvalleuPheThrglyThrMetArglyleuaspProPheasngllyHlsThr 1142
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 Oy 1163 ProglylyMetCaspThrgluLeuAlaglySerGlySeraspPheSerValygllyArg 1182
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 Oy 1203 AlathralaasnValaspProargThraspGluLeuIllegllylelyleArggluys 1222
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 Oy 1223 PheAlahlsCyseThrValleuThrlleAlahlsArglyleuasnThrlleleaspSerap 1242
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 Oy 1243 lylsileMetValleuaspSerGlyArglyleuysgluTyraaspGluProTyraalleu 1262
 Db 3542 NNN 3601
 Oy 1263 GlnasulysGluSerleuPheTyryllyMetValyGlnlyleuGlylysaAlagluAla 1282
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 Oy 1283 AlaleuThrgluThralalyglu 1290
 Db 3662 GCCCTCAGTGAACAGCAAAACAG 3685
 RESULT 5
 AK032802 LOCUS AK032802 3208 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720455a17
 product:ATP-binding cassette, sub-family C (CFTR/MRP), member 4
 homolog (Human), full insert sequence.
 AK032802.1 GI:26083045
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahigaki, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Onoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3208)
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirokane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsue, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takehashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suibyo-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
 URL: <http://genome.gsc.riken.jp/>
 URL: <http://fantom.gsc.riken.jp/>
 Location/Qualifiers

FEATURES
 source
 1. 3208
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:6720455A17"
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 1. 3208
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misc_feature

1. 3208
 /note="ATP-binding cassette, sub-family C (CFTR/MRP), member 4 homolog (Human) (SWISSPROT:O15439, evidence: FASTA, 86.9%ID, 98.1%length, match=3904)"

ORIGIN

Alignment Scores:

Pred. No.: 1.82e-277 Length: 3208
 Score: 2582.00 Matches: 502
 Percent Similarity: 95.3% Conservative: 21
 Best Local Similarity: 91.4% Mismatches: 26
 Query Match: 38.0% Gaps: 0
 DB: 4

US-09-976-858-42 (1-1325) x AK032802 (1-3208)

Qy 777 Leuphegiyllealargserleuvalpheyvalleuvalasenserserlnhr 796
 Db 2 CTTTGGCAHRCAGATCCCTACTGGTGTCTATATCTTGTAAGCTTCCAGACT 61
 Qy 797 Leuhisaenlysmetphegluserlleuvalaprovallleuphepaphan 816
 Db 62 TTGCACACAGAGATTTGATCCATCATCGAAGCTCCCGTGTCTTTCGACAGAAAT 121
 Qy 817 Protlegiyaglleuvalaspheserlyabaplleghyaleuvalasphleu 836
 Db 122 CCATCCGAGAGATTTAAATCGTTCTCCAAAGCATCGACATGATGATTTGCTT 181
 Qy 837 Proleuthrphleuaspheileghlnhrleuvalvalaiglyvalaserv 856
 Db 182 CCCCTGAGCTTCTGACTTCTATCCAGAGCTTCTCTGTAAGTGTGCTG 241
 Qy 857 Alavalalavalaleprotriplealaleproleuvalproleuglylellephele 876
 Db 242 GCCCGGCGGATCCCTTGATCTCATACATTCGCTCGCTCGCTGCTTCTG 301
 Qy 877 Pheleuagatgtyrphleuagluhrseratgarpvallyabxleuaglserserthr 896
 Db 302 GTTCTTCCGAGATCTTCTAGAGAGCTCACCGGATGTCAAGCGCTGAATCCACA 361
 Qy 897 Argserprovalpserhisleuserserserleugnglyleuvaltrthrleargla 916
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 Qy 917 TyrlvalagluagluarCyseglngluuupheapalalaleglasphleuhserseru 936
 Db 422 TACAAAGTGAAGAGAGTGTCAAGAGCTGTTGATGACACACAGAGATTCATCAAG 481
 Qy 937 AlaTrpPheleuPheleuThrsersargrtrpheaialavalxleuapalaleCys 956
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Db 602 GGGCAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 661
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 Db 1142 GAGGCAATGAG 1201
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 Qy 1237 ThrIleleYleYleYleYleYleYleYleYleYleYleYleYleYleYleYleY 1256
 Db 1382 ACCATCATGACAG 1441
 Qy 1257 GluProYleYleYleYleYleYleYleYleYleYleYleYleYleYleYleYleY 1276
 Db 1442 GAGCGATGTCTGCTGCAAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501
 Qy 1277 GlyYvalagluYalalalaleuThrYleYleYleYleYleYleYleYleYleY 1296
 Db 1502 GCGAAGGCGAG 1561
 Qy 1297 TyrProHisIleYleYleYleYleYleYleYleYleYleYleYleYleYleYleY 1316
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 Qy 1317 ThrleuThrIlePhegluThralaleu 1325
 Db 1622 GCCTTAACATATTTGAAGAGCATTTG 1648

RESULT 6
 AK029876
 LOCUS

AK029876 5920 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931419N09 product:ATP-binding cassette, sub-family C (CFTR/MRP), member 1a, full insert sequence.

ACCESSION AK029876

VERSION AK029876.1 GI:26325799

KEYWORDS HTc; Cap trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

JOURNAL PUBMED 10349636

REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL PUBMED 11042159

REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watanabe, M., Yonekura, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL PUBMED 11076861

REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

JOURNAL PUBMED 11076861

REFERENCE 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 563-573 (2002)

JOURNAL PUBMED 11076861

REFERENCE 6 (bases 1 to 5920) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submissions Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
source
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ORIGIN
Alignment Scores:
Prod. No.: 3,94e-241 Length: 5920
Score: 2263.00 Matches: 491
Percent Similarity: 57.3% Conserved: 288
Best Local Similarity: 36.1% Mismatches: 468
Query Match: 33.3% Indels: 112
DB: 4 Gaps: 23

US-09-976-858-42 (1-1325) x AK029876 (1-5920)

QY 3 ProvalTYrGInGInuVal-----LysProaenProLeuGInaSPAlaSnleu 18
|||||:|||||
DB 625 CCCCTGTTCTGTAACGTCAGACGGAATCATGCCAGATCCAGAGCCCTTTC 684
19 CysSerArgValPhePhTYrTLeuSnProLeuPhelylleglyHilLyeArgArg 38
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DB 685 CTTTCAGAGATTACTTCTGGTGGATTA CAGGAGATGAGTGCACGGCTGACGCCGCC 744
39 LeuGInGInuAPaPMeTYrSerValLeuProGInuAPaPArgSerGInHileuGly 58
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DB 745 CTGAGAGACAGTACTCTGTCATTGAATTAAGAGGACACATCAGAAAGAGTACT 804

QY 59 GluLeuGlnGlyPheThrAspLeu----- 67
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 DB 805 GTGCTGTGAATTAATCGAAGAGAAATGATTAAGTCAAGAGACGCTGTACGATT 864
 QY 67 ----- 67
 DB 865 GTGTATGCCCTCCCAAGATCCAGCAAGCTTAAGGAAATGCCAGTTGATGTGAAT 924
 QY 68 -----ValleuArgAlaGluAsnAspAlaGlnLysProSerLeuThr 81
 DB 925 GAGGAGGTGAGGACCTGATTGTCAAGTCAAGCTCCCAAGAGATCGGAGAGCCCTCTGTTC 984
 QY 82 ArgAlaIleIleLysCysThrTrpLysSerTyrLysValLeuGlyIlePheThrLeuIle 101
 DB 985 AAGGTTTATACAAAGCTTTGTGCTCCCTACCTCTCCATGAGCTTCTGTACAAAGCCCTT 1044
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 DB 1105 GACGAGAGGCTCCGACTGG-----CAGGCTACTTTTACACAGCACTGGT 1152
 QY 142 ThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGlnCys 161
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 Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 5899)
 Koehler, K., Beyer, A., Mewes, H. W., Weil, B., Amid, C., Oanger, A.,
 Fobo, G., Han, M., and Wiemann, S.
 The German cDNA Consortium
 Direct Submission
 Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr. 1, D-85764
 Neudorf, GERMANY
 COMMENT
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
 Sequenced by BMFZ (Biomedical Research Center at the
 Heinrich-Heine-University, Duesseeldorf/Germany) within the cDNA
 sequencing consortium of the German Genome Project. This clone
 (DKFZp781G125) is available at the RZPD Deutsches Ressourcenzentrum
 fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD
 for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp781G125
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
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ORIGIN

Alignment Scores:

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US-09-976-858-42 (1-1325) x CR749835 (1-5899)

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Db 2544 GCGCTGGGCAATTTCAAGAGGATGCGCGTG-----TTTGGCTATCTCATGCGC 2591

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Oy 1262 LeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGly-----Lys 1278
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Oy 1279 AlaGlnAlaAlaAlaLeuThrGluThrAlaLysGlnValTyr-----PheLysArg 1295
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RESULT 8
LOCUS BC046560 4547 bp mRNA linear HTC 19-NOV-2003
DEFINITION Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member 3, mRNA (cDNA clone IMAGE:4194166), containing frame-shift errors.
ACCESSION BC046560
VERSION BC046560.1 GI:28279835
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 4547)
Straussberg, R.L., Collins, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schermer, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schermer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, S.L., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stephenson, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L.,
Schermer, T.E., Brownstein, M.J., Uedini, T.B., Toshiyuki, S.,
Abramson, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J.,
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Wolfe, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whiting, M., Madan, A., Madan, A., Rodriguez, S.,
Bohlander, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Buetow, K.H., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length

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JOURNAL human and mouse cDNA sequences
PROC. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCES 2 (bases 1 to 4547)
AUTHORS Straussberg, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cga@bbs.fda.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
Kowls, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nantavat,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/BLAT at: http://image.llnl.gov
Series: IRAX Plate: 92 Row: F Column: 22
This clone has the following problem: frame shifted.
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/strain="FVB/N"
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/clone_id="NCI CGAP_L19"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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Pred. No.: 5,866-228 Length: 4547
Score: 2144.00 Matches: 483
Percent Similarity: 56.4% Conservative: 283
Best Local Similarity: 35.6% Mismatches: 479
Query Match: 31.6% Indels: 114
Gaps: 24
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Oy 23 PhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysValArgLeuGluGluAsp 42
Db 220 TCTTTCGTGTGTTCACAAAGCTTGCATCTTGGTCAACGATGCTCCCTGAGAGACCGT 279
Oy 43 AspMetTyrSerValLeuProGluAspArgSerGlnHisLysGlnGluGlnGlnGly 62
Db 280 GACCTCGGTCTGTCTGAGAGAGACTGCTCTCAAGAGTGTACAAAGCGGCTGTGAA 339
Oy 63 PheTrpAspLysGlu-----ValLeuArgAlaLeuAsnAlaGlnLysProSerLeu 67
Db 340 GCATGCAAAAGCAGACCAAGCATCAGGCTCCAGACGCAAGCATGAGCAAG 399
Oy 68 -----ValLeuArgAlaLeuAsnAlaGlnLysProSerLeu 80
Db 400 ATCCAGAGTGAAGATGCGGTCTTCAAGCCGACCAAGCATCAGACCTTCTT 459
Oy 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100

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 QY 121 GluAsnIlePhePheMetAspSerValAlaLeuAsnIlePheVal 135
 Db 580 TCT-----GACCCC-----ACGGCCCCACCTGGTGGGGCTTC 612
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 QY 156 PheIleHisValIleCysValIleIlePheIlePheIlePheIlePheIleIlePheIle 175
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OY 1242 pLysLleMetValLeuAspSerGlyArgLeuLysGlnTrpAspGluProTyValLeuLe 1262
Db 4026 CAGGCTCTGCTTGTGACCAAGAGATGACTGAAATTTGATTTCTCCAGTCAACTCAT 4085
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CL969772 4953 bp DNA linear GSS 21-SEP-2004
LOCUS OSIFC018842 Oryza sativa Expressed Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL969772
VERSION CL969772.1 GI:52394164
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiales; Oryzoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 4953)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
JOURNAL
COMMENT
CONTACT: Chen Chen
Department of Bioinformatic
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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ORIGIN
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Pred. No.: 2138.00 Matches: 481
Score:

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Percent Similarity: 56.1% Conservative: 266
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 Query March: 31.5% Indels: 88
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US-09-976-858-42 (1-1325) x CL969772 (1-4953)

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 DB 661 CTGGCTGGTGGGAGAGATTTGGCTTACG-----AGGCATGCTAATATATTTCCAGG 714

QY 22 ValPhePheTPTTLeuAsnProLeuPheLYSileGlyHisLYeArgArgLeuGlu 41
 DB 715 AATATCTTTTCATGATGATGATCTCTTAATGCAACAGATTTTAAAGGCCCTACCCGAT 774

QY 42 AspAspMetLYSerSerValLeuProGluAspArgSerHisLeuGlyGluGln 61
 DB 775 AAGCATATTTGAAATTTACACAGTTGGGATGAGACTGAAACATTTGACACCACTTCCAA 834

QY 62 GlyPheTTPAspLYSGLuValLeuArgAlaGluAsnAspAlaGlnLYSProSerLeuThr 81
 DB 835 AATGCTGGAGACATGAGCTTCAAAA-----CCAAAGCTTGGGCTGTA 879

QY 82 ArgAlaIleIleLYSLeuCYSTyrTTPLeuValLeuGlyLYLePheThrLeu 101
 DB 880 CCGGCTCTGCATAGCAGCCTTGGTGGAGATTTTGGCTAGAGGATTTTAAAGATTGGC 939

QY 102 GlnGluSerAlaLYeValIleGlnProIlePheLeuGlyLYSileLeuAsnTYrPheGlu 121
 DB 940 AATGATCTTCTCATGTTTGTGGCCCATCATATTTGAACTTGTGGAGTCTATGCA 999

QY 122 AsnTYrAspProMetAspSerValAlaLeuAsnThrAlaTYrAlaThrValLeu 141
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QY 181 LeuSerAsnMetAlaMetGlySerThrThrThrGlyGlnIleValAsnLeuSerAsn 200
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 DB 1642 CTGCTGGAGAGTACTTACACACAGCAAAAGGCTTTCATCATCTTCACTTGTCTGCTC 1701

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QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuAspGlu-----Ile 395
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QY 436 ArgProGlyGluLeuAlaValValGlyProValGlyAlaGlyLYSLeuSerSerLeuLeu 455
 DB 1924 CCTATGGSCAGTTTGTGCAATGATGAGAAAGCACTGGGAGGGAGAGACTTCTTATT 1983

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QY 493 IleLeuPheGlyLYSLeuTYrGlnLYSGLuArgTYrGlyLYSValIleLYSAlaCysAla 512
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QY 573 Leu----- 573

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QY 591 ThrHisGlnLeuGlnTYrLeuLYSAlaIleAspGlnIleLeuIleLeuLYSAspLYS 610
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TITLE A scan for positively selected genes in the Genomes of Humans and Chimpanzees
 JOURNAL (er) Plos Biol. 3 (6), E170 (2005)
 PUBMED 15869325
 REFERENCE 2 (bases 1 to 4638)
 AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES
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 Score: 2046.50 Matches: 466
 Percent Similarity: 53.9% Conservative: 258
 Best Local Similarity: 34.7% Mismatches: 499
 Query Match: 30.2% Indels: 119
 DB: 11 Gaps: 19

US-09-976-858-42 (1-1325) x DQ044660 (1-4638)

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 QY 54 GINHSLVGLYGLUGLULUENGLNGLYPHETPRAPRYGLVALLEUARGLA----- 71
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 QY 71 ----- 71
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 DB 826 TTGAACAAGAAATCAGAGTCAAGCCAAAGATGCCCTTGTCTGGAAGATGTTGAAAGAA 885
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 DB 886 AAAAAGAACTGGGAGCCAAAGATGTTCCAAATCTGTGATGTAAGGCTCTGTTCC 945
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genomic survey sequence.
ACCESSION D0038460
VERSION D0038460.1 GI:66889669
KEYWORDS GSS.
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ORGANISM Homo sapiens
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Hominiidae; Homo.
1 (bases 1 to 4080)
REFERENCE Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 4080)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Best Local Similarity: 35.1% Mismatches: 480
Query Match: 30.1% Indels: 141
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VERSION   AY407265.1 GI:39763236
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 4185)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene tritos
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302

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REFERENCE 2 (bases 1 to 4185)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
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 Db 2305 NNN 2364
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 Db 2365 CAGCTG-----GAGAGAAAGCGAGGCTTCAAGTCCCTGCTCAGTATATGCT 2412
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 QY 720 LeuAsnThrAlaAlaGlnValAlaTrpValLeuGlnAspTrpTrpLeuSerTrpAla 739
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 QY 740 AsnLysGlnSerMetLeuAsnValThrValAsnGlyGlyAsnValThrGluLysLeu 759
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 Db 2758 TTTGACAGACCCCAAGAGAGATCTCAACAGGTTTCCAAAGACATGATGAAGT 2817
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Db      2878 TGTGTGGGAATGATCGAGAGTCTTCCGTTGCTTGTGCGAGTGGCGCCCTTGTCTC
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      2938 ATCCCTTTTTCAGTCTGACATTTGTCTTCACAGGTTCTGATGTGGAGCTGAAGGCTG
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      913  ThrIleArgAlaIleTyr--LysAlaGluGlu-----ArgCysGlnGluLeuPheAsp
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      3118 GACAAACCA-----GCTCCTTTTTTTGTGTTACGTGTGCGCATGCGGTGGCTG
      949  AlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeu
      3166 GCTGTGCGGCTGTGACCTATCAGCATTCGCCCTCATCACACACAGGGGCTGATGATGCTT
      969  IleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThr
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      989  LeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGlnAspMetMetIle
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      3766 ATTGTGGAGCTCCGTGAGAGGACACACATGAAGAAATGATTGCTCAGCTACCTCGAAA
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      3826 CTTGATATCTGAAGTGTGAGATGGGATTAACCTTCTCAGTGGGAGAGCGGAGCTCTTG
      1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla
      3886 TGCATATGCTAGAGCCCTGCTCCGCCACTGTAAAGATTCTGATTTTATAGTAAAGCACAGT
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      4006 TGTACATGCTGACCATTTGCCCATTCCTCGACACAGGTTTCAGAGCTCGATAGATTATG
      1246  ValLeuAspSerGlyArgLeuLysGluIleTyrAspGluProTyrValLeuLeuGlnAsnLys
      4066 GTGCTGCGCCAGGACAGAGTGTGAGATTGACACCCCATCGGTCTCTGTCCAAACGAC
      1266  GluSerLeuPheTyrLysMet
      4126 AGTTCCGATTCATGCCATG
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      ACCESSION  AY407267
      VERSION   AY407267.1 GI:39763238
      KEYWORDS  GSS.
      SOURCE    Mus musculus (house mouse)
      ORGANISM  Mus musculus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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      Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
      Adams,M.D. and Cargill,M.
      TITLE      Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
      Adams,M.D. and Cargill,M.
      Inferred nonneutral evolution from human-chimp-mouse orthologous
      gene trios
      JOURNAL    Science 302 (5652), 1960-1963 (2003)
      PUBMED    14671302
      2 (bases 1 to 4176)
      Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
      Adams,M.D. and Cargill,M.
      TITLE      Direct Submission
      JOURNAL    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
      Rockville, MD 20850, USA
      COMMENT    This sequence was made by sequencing genomic exons and ordering
      them based on alignment.
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      /mol_type  "genomic DNA"
      /db_xref   "taxon:10090"
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      /gene="ABC5"
      /locus_tag="HMC2833"
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      Alignment Scores:
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      Score: 1957.50 Matches: 469
      Percent Similarity: 51.7% Conservative: 235
      Best Local Similarity: 34.4% Mismatches: 522
      Query Match: 28.8% Indels: 137
      Gaps: 26
      DB:
      US-09-976-858-42 (1-1325) x AY407267 (1-4176)
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      30  ::::::::::::::::::::
      Db      157 CACCAAGTGGCAAAAGCTGAGACTTTCTCTACATGACACCTTTTCATGCTCTCTCTG
      216  ::::::::::::::::::::
      QY      31 PheLysIleGlyHisLysArg--ArgLeuGlnGluLysAspAspMetTyrSerValLeuPro
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DB 337 GAAGTTGGGCGCAGAGCT-----GCCCTCCCGGAAGGGTTGTGTGATCTTTTGC 387
QY 90 LysSerTyrLeuValLeuGlyIlePheThrLeu---IleGluGluSerAlaLysValIle 108
DB 388 CGCACAGAGCTCATCTGTGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 447
QY 109 GlnProIlePheLeuGlyLys---IleIleAsnTyrPheGluAsnTyrAspProMetAsp 127
DB 448 GGACGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 489
QY 128 SerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIle 147
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QY 148 -----LeuAlaIleLeuHisIleLeuTyrPheTyrHisVal 159
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QY 260 SerLeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluVal 279
DB 886 TATTTCAGGAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 945
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DB 946 CTACTCTCATTTAAATTCATTAAATGTATGTCTGGGTCTAAAGCGTTTCTCAGTGTGTG 1005
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QY 421 ----- 421
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QY 422 -----AlaSerGluThr 425
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QY 426 Pro----- 426
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DB 1591 AACTGTCAACATTGACTTGAATTAAGAGGGCAAACTGTGTGTGTGTGTGTGTGTGTGT 1650
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 VERSION CL957124.1 GI:52369499
 KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
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 REFERENCE 1 (bases 1 to 4483)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Gao, M., Xiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G., K. S., Deng, X. W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
 Unpublished (2004)
 CONTACT Chen Chen
 JOURNAL
 COMMENT Department of Bioinformatic
 Beijing Institute of Genomics


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Db      2440 GCTGATCTTATTCGTGCATGAAAGGTGGAGAAATGACAGAGCGCAAAATATACGAA 2499
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Db      2500 ATACTGTGATCAGGGAGAGATTCAATGAACTGTGTGCTCACAGAGACTCTTACC 2559
Qy      640 GlnProValProGlyThrProThrLeuArgAsnArgThrPheSerGlySerVal 659
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Qy      936 uAlaTrpPheLeuPheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCy 956
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RESULT 15
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 VERSION CL970490.1 GI:52395588

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 Job time : 11411 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2006, 09:29:33 ; Search time 515 Seconds
(without alignments)
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Perfect score: 6767
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Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	6760	99.6	6082	3	US-09-685-166A-535
5	6760	99.6	6082	3	US-09-679-426-535
6	6760	99.6	6082	3	US-09-759-143-535
7	6760	99.6	6082	3	US-09-651-236-535
8	6760	99.6	6082	3	US-09-657-279-535
9	6760	99.6	6082	3	US-10-012-896-535

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11	6600.5	97.3	6140	3	US-09-636-215-536	Sequence 536, App
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17	6600.5	97.3	6140	3	US-10-012-896-536	Sequence 536, App
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ALIGNMENTS

RESULT 1
US-09-647-140B-1
; Sequence 1, Application US/09647140B
; Patent No. 6803184
GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruth, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
TITLE OF INVENTION: MRP-related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
FILE REFERENCE: FCCC 98-02
CURRENT APPLICATION NUMBER: US/09/647,140B
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: PCT/US99/06644
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,759
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/095,153
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 4231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-647-140B-1
Alignment Scores:
Pred. No.: 0
Score: 6779.00
Percent Similarity: 99.94
Length: 4231
Matches: 1323
Conservative: 1

Best Local Similarity: 99.8% Mismatches: 1
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 QY 41 GluAspAspMetTySerValLeuProGluAspArgSerGlnHisiLeuGlyGluLeu 60
 DB 236 GAAAGATGATGATGATTCAGTGTGCGCAGAAAGCCGTCAAGACCTTGAGAGAGATTG 295
 QY 61 GlnGlyPheTrpAspIySgluValLeuArgIleGluAsnAspAlaGlnIySPProSerLeu 80
 DB 296 CAAGGCTTCTGGATTAAGAAAGTTTAAAGAGTGAAGATGACGCAAGAGCCCTCTTTA 355
 QY 81 ThrArgAlaIleIleIySeyTrpTrbIySPProIySPProIySPProIySPProIySPProIy 100
 DB 356 ACAAGGCAATCATTAAGGTGTAAGTAAATCTTATTAGTTTGGGAAATTTTACGTA 415
 QY 101 IleGluGluSerAlaIyValIleGlnProIlePheLeuGlyIySileIleAsnTyPhe 120
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 QY 121 GluAsnTyPhePProMetAspSerValAlaLeuAsnThrAlaTyAlaThrVal 140
 DB 476 GAAATTTATGATCCCATGATCTGTGGCTTGMAACAAGCGTACCCCTATGCCCGGTG 535
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 DB 536 CTGACTTTTGGACGGCTCATTTTGGCTTATGCTACATCACTTATTTTATCAAGTTCG 595
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 QY 261 LeuArgSerIySPProIySPProIySPProIySPProIySPProIySPProIySPProIy 280
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 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyIySleuTyGlu 500
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QY 701 TyrIysAsenTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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 QY 1321 PheGlnThrAlaLeu 1325
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RESULT 2
 US-09-439-313-535
 ; Sequence 535, Application US/09439313
 ; Patent No. 6329505
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yugu
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Soik, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-535

Alignment Scores:

Pred. No.:	0	Length:	6082
Score:	6760.00	Matches:	1324
Percent Similarity:	99.9%	Conservative:	0
Best Local Similarity:	99.9%	Mismatches:	1
Query Match:	99.6%	Indels:	1
DB:	3	Gaps:	0

US-09-976-858-42 (1-1325) x US-09-439-313-535 (1-6082)

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DB      786 GATGTGAACAAGTTTATCATCGGTGACAGGTCTTTCACCTCTGTGGGCAAGCAACACG 845
QY      221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyIlyleSerCySeuAlaGly 240
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QY      621 LeuIlyseSerGlyIleAspPheGlySerLeuLeuIlyIlyAspAsnGlnGluSerGlnGln 640
```


Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carver, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121, 42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-636-215-535

Alignment Scores:

Pred. No.:	0	Length:	6082
Score:	6760.00	Matches:	1324
Percent Similarity:	99.9%	Conservative:	0
Best Local Similarity:	99.9%	Mismatches:	1
Query Match:	99.6%	Indels:	0
DB:	3	Gaps:	0

US-09-976-858-42 (1-1325) x US-09-636-215-535 (1-6082)

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DB 426 ACAAGGACATCATTAAGTTAACTGGAATCTTATTTAGTTTGGAAATTTTTCGTTA 485
QY 101 IleGluGluSerAlaIysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140
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QY 141 LeuThrPheCyThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
DB 606 CTGACTTTTGGACGCTCATTTTGGCTATATGACATCACTTATATTTATACAGTTTCA 665

QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgIysAlaLeuArg 180
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QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyIysLeuPheSerSer 260
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RESULT 4
US-09-685-166A-535
; Sequence 535, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
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; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
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; APPLICANT: Wang, Aijun
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; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-535
Alignment Scores:
Pred. No.: 0 Length: 6082
Score: 6760.00 Matches: 1324
Percent Similarity: 99.9% Conservative: 0
Best Local Similarity: 99.9% Mismatches: 1
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DB: 3 Gaps: 0
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 QY 941 PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
 DB 3006 TTTTGGACAGCTCCCGTGTGCTCCCGTCCGTGAGATGCCATGTGTGCCATGTTTGT 3065
 QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnAlaGly 980
 DB 3066 ATCATCTGCTGCTTGGTCTCTGATTTCTGGCAAAAATCTGTGATCCGGGAGTGTGT 3125
 QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000
 DB 3126 TTGGCAGTCTCTAAGCCCTCAGCGTCAAGGGAGATTTTCAAGTGTGTGTGCAAAAGT 3185
 QY 1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
 DB 3186 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGTCATTTGAATACACAGACTTGA 3245
 QY 1021 LysGluAlaProTropGluTyrGlnLysArgProProAlaTyrProHisGluGlyVal 1040
 DB 3246 AAGAAAGCACTTGGGAATATACAGAAAGCCCAACAGCTGGGCCCAATGAGAGATG 3305
 QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
 DB 3306 ATAATCTTGAACAATGTAATCTCATGTACAGTCCAGGTGGGCTCTGTACTGAAGCAT 3365
 QY 1061 LeuThrAlaLeuIleLysSerGlnGlyLysValGlyIleValGlyArgThrGlyAlaGly 1080
 DB 3366 CTGACAGCACTCATTAATTCACAGAAAGGTGGTGCATTTGGGGAAGAACCGAGACTGGA 3425
 QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTyrPile 1100
 DB 3426 AAAAGTTCCTCATTTCCAGCCCTTTTGAATTTGTGCAGAACCGAAGGTAAATTTGAT 3485
 QY 1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
 DB 3486 GATAAGACTTGCACAACTGAATTTGACCTTCAAGATTTAAGGAAGAAATGCAATCATTA 3545
 QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
 DB 3546 CCTCAGGAACCTGTTTGTCTCAGTGAACAAATGAGAAACCTGTGATCCCTTATATAG 3605
 QY 1141 HisThrAspGluGluLeuTyrAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160

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DB 3606 CACACGGATGAGGAAGCTGTGGAATGCTTACAGAGGTCAACCTTAAGAAACCAATTGAA 3665
QY 1161 AAPLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPhseValGly 1180
DB 3666 GATCTTCTCGTAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 3725
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
DB 3726 CAAAGCAACTGGTGTGTGCTTGCACAGGGCAATTCAGAGAAATCAGATATTATTTATTT 3785
QY 1201 AAPGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
DB 3786 GATGAGACGACGCAAAATGTGATCCAGAACTGAAAGATTAATCAAAAAAATC-CGG 3844
QY 1221 GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
DB 3845 GAGAAATTTGGCCACCTGCAACCGTGTACCACTTGGCACAGATGAAACCACTTATTGAC 3904
QY 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
DB 3905 ACGCAACAAATATGTTTATGATTACAGAAAGCTGAAAGAAATATGATGAGCCGTATGTT 3964
QY 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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QY 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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QY 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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QY 1321 PheGluThrAlaLeu 1325
DB 4145 TTGAGACAGCACTG 4159

RESULT 5
US-09-679-426-535
Sequence 535, Application US/09679426
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darwick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-679-426-535
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Alignment Scores:
Pred. No.: 0 Length: 6082
Score: 6760.00 Matches: 1324
Percent Similarity: 99.94 Conservative: 0
Best Local Similarity: 99.94 Mismatches: 1
Query Match: 99.68 Indels: 1
DB: 3 Gaps: 0

US-09-976-858-42 (1-1325) x US-09-679-426-535 (1-6082)

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QY 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
DB 246 CCGCGTCTTCTGTGTGCTCAATCCCTGTTTAAATTTGGGCANAAACGGAGATTAG 305
QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
DB 306 GAAAGATGATATGATATTACGTGCTGCAGAAACCGCTCACAGCACTTGAGAGAGATTG 365
QY 61 GlnGlyPheTyrPheLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
DB 366 CAAGGTTCTGGAGTAAAGAGTTTAAAGCTGAGAAATGACGACAGAACGCTTCTTTA 425
QY 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
DB 426 ACAAGACAAATCATTAATGTTTACGAAATCTTATTTAGTTTGGAAATTTTACGTTA 485
QY 101 IleGluGlnSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
DB 486 ATTGAGAAAGTGCAGAAATTAATCCAGCCCATATTTTGGAAAAATTAATTAATTTT 545
QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrAlaThrVal 140
DB 546 GAAATTTATGATCCCATGATTTCTGTGCTTTGAAACAGCGTACGCTATGCGCCAGG 605
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
DB 606 CTGACTTTTTCACACCTCATTTTGGCTATCTACGATCACTTATATTTTATACACTTAC 665
QY 161 CysAlaGlyMetCysArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
DB 666 TGTGCTGGATGAGGTATCAGATAGCCATGAGCCATATGATTTATCGGAAGCACTTGT 725
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
DB 786 GATGGAACCAATTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGAGAGCACTG 845
QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyLysSerCysLeuAlaGly 240
DB 846 CAGGCGATCGCAGTACCTGCTTACTGATGAGATAGAAATATCGTCTGTGCG 905
QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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QY 261 LeuAspSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
DB 966 CTGAGAGATTAACCTGCACTTTCAGGATGCCAGATCAAGACCATTAATCAATTA 1025
QY 281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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QY 301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Qy 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrglyAla 360
Db 1206 CTCCTCGGAGTGTGATCAGACCGCGGTTGTGCGAGTGCATGCGTATGGGGCT 1265
Qy 361 ValAlaGluThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
Db 1266 GTCGCGCTGACCGGTAACTCTCTCTCTCCCTCAGCCATTCAGAGGGGTGCAGAGCCAAATC 1325
Qy 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
Db 1326 GTCACATCCGAGAAATCCAGACCTTTTGTCTACTTGAATGAAATACAGAGCAACCGT 1385
Qy 401 GlnLeuProSerAspGlyValIleYsMetValHisValGlnAspPheThrAlaPheTrpAsp 420
Db 1386 CAGCTCGCGTCAAGATGTAAGTAAGATGTCATGTCAGAGATTTTACTCTTTTGGAT 1445
Qy 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
Db 1446 AAGCATCAGAGACCCCAACTCTACAGAGCGCTTCTCTTACTGTCAGACTGGCAATG 1505
Qy 441 LeuAlaValValGlyProValGlyValIleGlySerSerLeuLeuSerAlaValIleGly 460
Db 1506 TTAGCTGTGTCGCGCCCGTGGAGCGAGGAGTCACTGTAAATGCCCTGCGCGG 1565
Qy 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrrValSerGln 480
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Db 1626 CAGCCCTGGGTGTTCTCGGGAACCTCGAGGAGTAATATTTATTTGGGAAAGAAATACGA 1685
Qy 501 LysGluAlaGlyTyrgluValIleIleYsAlaCysAlaLeuValYsAspLeuGlnLeuLeu 520
Db 1686 AAGGAAACATAGAAAAGTCAATAAGGCTGTGCTGAAAAGAAATTTACAGCTGTG 1745
Qy 521 GlnAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnYs 540
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Db 1866 CCTTCAGTGCAGTGTGATCGGAGATGACAGACACTGTTCGAACCTGTGTATTTGTCA 1925
Qy 581 IleLeuHisGluValIleThrIleLeuValThrHisGlnLeuGlnTyrrLeuYsAlaIle 600
Db 1926 ATTTGTCATGAGAAAGTCAAAATTTTATGACTCATGCTCAGTCTCAGTCAAGCTGCA 1985
Qy 601 SerGlnIleLeuIleLeuYsAspGlyYsMetValGlnYsGlyThrTyrrThrGluPhe 620
Db 1986 AGTCAGATTCTGATTTGTAAGATGTAAGATGTCAGAGGAGCTTACCTGAGTTC 2045
Qy 621 LeuYsSerGlyIleAspPheGlySerLeuLeuYsValYsAspAsnGluGlnSerGluGln 640
Db 2046 CTAAATATCTGATATGATTTTGGCTCCCTTTAAAGAGATTAAGAGAAAGTCAACAA 2105
Qy 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
Db 2106 CTTCCAGTTCAGAAATCTCCACATCAAGAAATCGTACTTCTCAGAGCTTCGCGTGG 2165
Qy 661 SerGlnGlnSerSerArgProSerLeuYsAspGlyAlaLeuGlnIleSerGlnAspThrGlu 680
Db 2166 TCTCAACATCTTTTATGACCTCTTGAAGATGGTCTCTGAGAGCCCAATGACAGG 2225

Qy 681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyValGlyPheGlnIle 700
Db 2226 AATGTCAGATTAACCTATCAGAGAGAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCG 2285
Qy 701 TyrrYsAsnTyrrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
Db 2286 TATAGAAATTAATCTCAGAGCTGTGTCATGAGATTCCTTCAATTTCTTATCTCCCA 2345
Qy 721 AsnThrAlaAlaGlnValAlaTyrrValLeuGlnAspTrpTrpLeuSerTyrrTrpAlaAsn 740
Db 2346 AACCTGAGCTCAGAGTTCCTATGTGCTTCAAGATGTGTGCTTTCATCTGAGGCAAC 2405
Qy 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyYsAsnValThrGluYsLeuAsp 760
Db 2406 AATCAAGATGCTAAATGCTCACTAAATGAGAGAAATGTAAACGAGAACTGAT 2465
Qy 761 LeuAsnTrpTyrrLeuGlyIleTyrrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
Db 2466 CTTAATCTGATCTTAAGAAATTAATCAGATTAACTGATTAACGCTTCTTTTGGCATA 2525
Qy 781 AlaArgSerLeuLeuValPheTyrrValLeuValAsnSerSerGlnThrLeuHisAsnYs 800
Db 2526 GCAGATCTCTATGTGATTCCTACGCTCCTGTAACTCTTCACAAACTTTCACAAACAA 2585
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Db 2586 ATGTTTGATCAATTTCAAAAGCTCCGGTATTAATTTTGTATAGAAATCCATATAGAA 2645
Qy 821 IleLeuAsnArgPheSerIleYsAspIleGlyHisLeuAspLeuLeuProLeuThrPhe 840
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DB 3486 GATAAGATCTTGACAACTGAAATTTGACCTTCAAGATTAAAGAGAAAATGTCAATCATA 3545
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DB 3546 CCTCAGGAACCTGTTTGTTCACCTGGAAACATGAGAAAACCTGGATCCCTTTATATAG 3605
QY 1141 HisThrAspGluGluLeuThrPasnAlaLeuGlnGluValGlnLeuysGlnThrIleGlu 1160
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DB 3666 GATCTTCCTGGTAAATGTAATCTGAATTTAGCAGATTCAGATCCAAATTTTGTGTGGA 3725
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
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QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysIleArg 1220
DB 3786 GATGAGCAACCGCAAAATGTGATCCAAAGACTGATGATTATACAAAATAATC-CGG 3844
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QY 1321 PheGluThrAlaLeu 1325
DB 4145 TTGAGACAGCACTG 4159

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RESULT 6

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US-09-759-143-535
; Sequence 535, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

```

```

; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepher, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-535
Alignment Scores:
Pred. No.: 0
Score: 6760.00
Percent Similarity: 99.9%
Best Local Similarity: 99.9%
Query Match: 3
DB: 3
Gaps: 0
US-09-759-143-535 (1-1325) x US-09-759-143-535 (1-6082)
QY 1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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QY 21 ArgValPhePheTrrPrrLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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DB 366 CAAAGGTTCTGGAATAAGAAAGCTTTTAAAGCTGGAATGACGCAAGAGCTTCTTTA 425
QY 81 ThrArgAlaIleIleLysCysTyrTrrPrrLysSerTyrLeuValLeuGlyIlePheThrLeu 100
DB 426 ACAAGAGCAATCATTAAGTGTACTGAAATCTTATTATTGTTTGGAAATTTTACGTTA 485
QY 101 IleGlnGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
DB 486 ATTTGAGAAAGTCCAAAGTATTCAGCCCAATTTTGGGAAAATTAATTAATTAATTTT 545
QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
DB 546 GAAAATTTATGATCCATGATTTCTGTGCTTTGAAACAGCGGTACGCTATGACCGGTG 605
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTrrHisValGln 160
DB 606 CTGACTTTTGGACGCTCATTTTGGCTATACGATCACTTATATTTTATCAGCTTACG 665
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
DB 666 TGTGCTGGGATGAGGTACAGGTACCAATGTGCTCATATGATTTATTCGAGAGCACTTGT 725
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlnGlnIleValAsnLeuSerAsn 200
DB 726 CTTAGTAACTATGGCCATGGGAGAGCAACCAAGGCGAGATGTCAATCTGTGTCACAT 785
QY 201 AspValaAsnLysPheAspGlnValThrValPheLeuHisIlePheLeuTrrPrrAlaGlyProLeu 220

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Db 786 GATGTGAACACAGTTGATCAGGTGACAGGTCTTACACTTCCTGCGGACAGACACTG 845
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 Db 846 CAGGGGATCGCAGTGCCTCCCTACTCTGATGAGATGAGATGAGATGCGCTTCGTGAG 905
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 Db 906 AAGGACGATCTATATCATTTCTCTGCGCTTGCAGAAAGCTGTTTGGAGAGTGTTCATCA 965
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 Qy 561 ProLeuSerAlaValAspAlaGluValSerArgIleLeuPheGluLeuCysIleCysGln 580

Db 1866 CCTCTCAGTGCAGATGATCGGAAAGTATGACAGACCTTGTTCGATCTGTATTTGCA 1925
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 QY 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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 DB 3786 GATGAAGCAGACGGCAAAATGTGATCCAGAACTGATGATTAATCAAAAAAATC-CCG 3844
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 RESULT 7
 US-09-651-236-535
 ; Sequence 535, Application US/09651236
 ; Patent No. 6818751
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Devin C.
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 ; APPLICANT: Jiang, Yugu
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 ; APPLICANT: Day, Craig H.
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 ; APPLICANT: Carter, Darlick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.42718C18
 ; CURRENT APPLICATION NUMBER: US/09/651,236
 ; NUMBER OF SEQ ID NOS: 865
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 535
 ; LENGTH: 6082
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-651-236-535
 Alignment Scores:
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 Score: 6760.00 Matches: 1324
 Percent Similarity: 99.98
 Best Local Similarity: 99.98 Mismatches: 1
 Query Match: 99.68 Indels: 1
 DB: 3 Gaps: 0
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 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlnGluLeu 60
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Qy      1121 ProGlnGlnProValaLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140
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Qy      1141 HisThrAspGlnGlnLeuTrpAsnAlaLeuGlnGlnValaGlnLeuLysGlnThrIleGln 1160
Db      3606 CACACCGAGTGAAGAACTGTGGAATGCTTACAAAGAGTACACTTAAAGAAACATTTGAA 3665
Qy      1161 AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValaGly 1180
Db      3666 GATCTTCTCGTAAATTAATGATGATGATTAAGACAGATTCAGATTCATTTTGTGTTGGA 3725
Qy      1181 GlnArgGlnLeuValaCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
Db      3726 CAAGAACAATGTGTGCTTGGCCAGGAGCAATTTCTCAGGAAATAATCAGATATTGATTATT 3785

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Qy      1201 AspGlnAlaThrAlaAsnValaAspProArgThrAspGlnLeuIleGlnLysIleArg 1220
Db      3786 GATGAAGGACGCGCAATGTGGATTCAGAGACTGATGAGTTAATCAAAAAAATATC-CGG 3844
Qy      1221 GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
Db      3845 GAGAAATTTGCCCATCTGACCGGTGTACATGTGACACAAATGGAACCACTTAATTTAC 3904
Qy      1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlnTyrAspGlnProTyrVal 1260
Db      3905 ACCGACAAATATATGTTTATGATTCAGAGAACTGGAAGATATGATGAGCCGATATGT 3964
Qy      1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrIaYMetValGlnGlnLeuGlyLysAlaGln 1280
Db      3965 TTGCTGCAAAATTAAGAGAGCCTATTTTACAAAGATGTGCAACCACTGGGCAAGCAGAA 4024
Qy      1281 AlaAlaAlaLeuThrGlnThrAlaLysGlnValaTyrPheLysArgAsnTyrProHisIle 1300
Db      4025 GCCGTGCCCTCCTCAGAAACGCAAAACAGGTATATCTCAAAAGAAATTTATCCACTATT 4084
Qy      1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
Db      4085 GGTCACTGACACCATGTGTTACAAACACTTCATATGACAGCCCTCACTTAATTAAT 4144
Qy      1321 PheGlnThrAlaLeu 1325
Db      4145 TTGAGACAGCACTG 4159

RESULT 8
US-09-657-279-535
; Sequence 535, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-279-535

Alignment Scores:
Pred. No.: 0
Score: 6760.00
Percent Similarity: 99.9%
Best Local Similarity: 99.9%
Query Match: 99.6%
DB: 3

Length: 6082
Matches: 1324
Conservative: 0
Mismatch: 1
Indels: 1
Gaps: 0

US-09-976-858-42 (1-1325) x US-09-657-279-535 (1-6082)

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 QY 21 ArgValPhePheTPTTLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGln 40
 Db 246 CCGGCTCTCTCTGGGCTCAATCCCTGTTTAAATGGCCATGAACGAGATTAGAG 305
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisIleGlnLysGluLeu 60
 Db 306 GAGAGATGATGATGATATTCAGTGTGCGCAGAGAACCGCTGCACAGACCTTGGAGAGAGTGG 365
 QY 61 GlnGlyPheTTPAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
 Db 366 CAAAGGTTCTGGGATTAAGAAGTTTAAAGCTGAGAAATGACGCAACGAAGCTTCTTTA 425
 QY 81 ThrArgAlaIleIleLysCysTyrTTPLeuPheSerTyrLeuValLeuGlyIlePheThrLeu 100
 Db 426 ACAAGAGCAATCATAAAGTTACTGGAATCTTATTTAGTTTGGGAATTTTACGTTA 485
 QY 101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
 Db 486 ATTTGAGGAAAGTGCCAAAGTAAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 545
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
 Db 546 GAAATTTATGATCCCATGATCTGTGCTTTGAAACACGCTACGCCCTATGCCACGGTG 605
 QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisIleLeuTyrPheTyrHisValGln 160
 Db 606 CTGACTTTTGGACGCTCATTTTGGCTATGATGCAATCACTTATATTTTATACCGTTGAG 665
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
 Db 666 TGTGTGGGATAGAGTTACAGATGACCATGTCATATGATTTATTCGAGGACACTTCCT 725
 QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlnIleValAsnLeuLeuSerAsn 200
 Db 726 CTTAGTAAATGCGCATGGGAGAGACACACACGCGCAGATGATCATCTGCTGTCAT 785
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTTPAlaGlyProLeu 220
 Db 786 GATGGAACAAGTTTGAATGACAGGTGACAGTCTTACACTTCTGAGGGCAGACACACTG 845
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTTPMetGlnIleGlyTyrLeuSerCysLeuAlaGly 240
 Db 846 CAGGGGATCGCAGTGACTGCCCTACTCTGATGAGATGAGAAATATCGGCTTGTGGG 905
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
 Db 906 ATGGCAGTTCTAATCATTTCTCTGCTTGCAGAAAGCTGTTTGGGAAGTTGTTCTCATCA 965
 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
 Db 966 CTGAGAGAGTAAACCGCAACTTTCACGATGCGACAGATCAGGACCATGAATGAAGTTA 1025
 QY 281 ThrGlyIleArgIleIleLysMetTyrAlaTTPGlyLysSerPheSerAsnLeuIleThr 300
 Db 1026 ACTGTATTAAGATATATAAAATGTAACGCTGGGAAAGTCAATTTTCAATCTTATACC 1085
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 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValIlePheValThrPheThrThrTyrVal 340
 Db 1146 TTGGCTTCTGTTTTCAGTCAAGCAAAATCATCGTTTGTGACCTTCAACCTACGACG 1205
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValIlePheValAlaValIleThrLeuTyrGlyAla 360
 Db 1206 CTCCTCGCAGTGTATCAACAGCCGCGTGTCTGCGCAGTGCAGCTGTATGGGGCT 1265

QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
 Db 1266 GTGGGCTGAGGGTTAACCTCTTCTTCCCTCAGCCATTTAGAGGGGTGCAGAGGCAATTC 1325
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
 Db 1326 GTCAACATCCGAAAGATCAGACCTTTTGGTACTGTATGAGATATCAACAGGCAACCGT 1385
 QY 401 GlnLeuProSerAspGlyLysLysMetValHisValIleAspPheThrAlaPheThrAsp 420
 Db 1386 CAGCTCGCTCAGATGATTAAGATGGTGCATGTGCAGATTTACTGCTTTTGGGAT 1445
 QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
 Db 1446 AAGCATCAGAGACCCCAACTCTAACAAGCCCTTCTTACGTCAAGCTGGCAATTG 1505
 QY 441 LeuAlaValValGlyProValGlyValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
 Db 1506 TTAGCTGTGTGCGCGCCGTGGAGCAGGAAATCATCATCTGTTAAGTCCGCTCGGG 1565
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
 Db 1566 GAATGGCCCAAGTCAGGGGCTGTCAGCTGCATGGAAGAAATGCCCTATGTGTCTCAG 1625
 QY 481 GlnProTTPValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500
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 QY 501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 Db 1686 AAGAACGATATGAAAAAGTCATAAAGGCTGTGCTCGAAAAAGATTACAGCTGTGG 1745
 QY 521 GluAspArgAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
 Db 1806 GCAAGGATTAACCTTGCAGAGAGAGCTGTATCAAGATGCTGACATCTATCTCTGAGCAT 1865
 QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlnLeuCysIleCysGln 580
 Db 1866 CCTCTCAGTGCAGTGTGATGCGGAAGTTAGCAGACACTTGTGCAACTGTGTATTTGTCAA 1925
 QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaIle 600
 Db 1926 ATTTGCAATGAGAGATCAAAATTTAGTCACTCATCGTTGCACTTCAAACTGCA 1985
 QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
 Db 1986 AGTCAGATTCGATTTTAAAGATGTGTAATGTGTGCAGAAAGGGACCTTACCTCAGATTC 2045
 QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluLysSerGln 640
 Db 2046 CTTAAATCTGGATATGATTTTGGCTCCCTTTTAAAGAGATTAATGAGAGAAAGTTTCA 2105
 QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTTP 660
 Db 2106 CCTCAGTTTCCAGGAACCTCCACACTTAAGATGTGATCTTCTCAGACTCTTGGTTGG 2165
 QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGlu 680
 Db 2166 TCTCAACATCTTCTAGACCTTCTTGAAGATGTGTCTCGAGAGCCAGATACAGAG 2225
 QY 681 AsnValProValThrLeuSerGluLysAsnArgSerGlnGlyLysValGlyPheGlnAla 700
 Db 2226 AATGCTCCAGTTTACCTATCAGAGAGAAACCGTTCTGAAAGAGAAAGTTTTCAGAGCC 2285
 QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisThrIleValIlePheIlePheLeuIleLeuLeu 720
 Db 2286 TATAAGATTAATCTCAGAGCTGTGTCTCAGATGTCTTCAATTTTCTTATTTCTCTTA 2345
 QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTTPLeuSerTyrTTPAlaAsn 740

Db 2346 AACACGACGAGCTCAGGTCCTATGTCCTTCAAGATTGGTGGCTTTCATACAGGCGCAAC 2405
 QY LysGlnSerMetLeuAsnValThrValaAngIyGlyValAsnValThrcIuIySLeuAsp 760
 Db 2406 AAACAAGATGCTAAATGCTACTGTAAATGAGGAGAAATGTAACTCAAGACCTAGAT 2465
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 Db 2466 CTAACTGGTACTTGAAGATTATTCAGGTTTACGTACGTACCTCTTTTGGCANA 2525
 QY AlaArgSerLeuLeuValaPheTyrValaLeuValaAsnSerGlnThrLeuHisAsnLys 800
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 QY LysGluAlaProTrpIuTyrGlnLysArgProProAlaTrpProHisGluGlyVala 1040
 Db 3246 AAAGAAGACCTTGGGAAATATCAAGAACGCCACACAGCCTGGCCCCCATGAAGAGTG 3305
 QY IleIlePheAspAsnValaAsnPheMetTyrSerProGlyGlyProLeuValaLeuLysHis 1060
 Db 3306 ATAAATCTTTGACAAATGTGAATTCATGTACAGTCCAGGTGGGCTCTGTGATCAAGACAT 3365
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 Db 3366 CTGACAGCACTCAATTAAATCAAGAAAGGTTGGCATTTGGGAAAGAACCGAGCTGGA 3425
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Db 3426 AAAAGTCCCTCAGCTCAGCCCTTTTAGATTGTGCAGAACCCGAAAGTAAAAATTTGATT 3485
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 QY HisThrAspGluGluLeuThrAsnAlaLeuGlnGluValaGlnLeuLysGluThrIleGlu 1160
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 QY PheGluThrAlaLeu 1325
 Db 4145 TTGAGACAGCACTG 4159

RESULT 9
 US-10-012-896-535
 / Sequence 535, Application US/10012896
 / Patent No. 6943236
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / APPLICANT: Dillon, David C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yugu
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Aijun
 / APPLICANT: Skeiky, Yaseir A.W.
 / APPLICANT: Hepley, William T.
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.

/ APPLICANT: Houghton, Raymond L.
 / APPLICANT: Vinals de Bassols, Carlota
 / APPLICANT: Foy, Teresa
 / APPLICANT: Panger, Gary R.
 / APPLICANT: Mananabe, Yoshinori
 / APPLICANT: Meagher, Madeleine Joy
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 / FILE REFERENCE: 210121.427C27
 / CURRENT APPLICATION NUMBER: US/10/012,896
 / CURRENT FILING DATE: 2001-12-10
 / NUMBER OF SEQ ID NOS: 1011
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 535
 / LENGTH: 6082
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-10-012-896-535

Alignment Scores:

Pred. No.: 0 Length: 6082
 Score: 6760.00 Matches: 1324
 Percent Similarity: 99.9% Conservative: 0
 Best Local Similarity: 99.9% Mismatches: 1
 Query Match: 99.6% Indels: 1
 DB: 3 Gaps: 0

US-09-976-858-42 (1-1325) x US-10-012-896-535 (1-6082)

QY 1 MetLeuProValThrGlnGluValIysProAsnProLeuGlnAspAlaAsnLeuCySer 20
 Db 186 ATGCTGCCCGTGTACAGAGAGGTGAAGCCCAACCCGCTGACAGACCGCACTCTGCTCA 245
 QY 21 ArgValPhePheTrpLeuAsnProIleuPheValIleGlyHisIleValArgArgLeuGlu 40
 Db 246 CGCGGTCTCTCTGCGTGCCTCAATCCCTGTTAAATGGCCATTAACGAGATTAGAG 305
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisIleuGlyValIleu 60
 Db 306 GAAGATGATATGATATTCAGTGTGCGCAGAAAGCCGCTCACACCTTGGAAGAGAGTTG 365
 QY 61 GlnGlyPheTrpAspLysGluValIleuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
 Db 366 CAAGGTTCTGGGATTAAGAAAGTTTAAAGCTGAGAAAGACGACAGAGCCCTCTTTA 425
 QY 81 ThrArgAlaIleIleIysCysTyrTrpLysSerTyrLeuValIleuGlyIlePheThrLeu 100
 Db 426 ACAAGAGCAATCATAAAGTGTACTGAAATCTTATTAGTTTGGAAATTTTACGTTA 485
 QY 101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyValIleAsnTyrPhe 120
 Db 486 ATTTGAGAAAGTGCACAAAGTAAATCCAGCCCATATTTTGGAAAAATTAATTAATTTT 545
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
 Db 546 GAAATTTATGATCCCATGATTTCTGTGCTTTGAAACAGCGTACGCTTATGCCAGGTTG 605
 QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
 Db 606 CTGACCTTTTGGACGCTCATTTTGGCTATACGACATCACTTAATTTTATACAGCTTCA 665
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
 Db 666 TGTGTGGGATAGAGTTACAGATAGCCAGTGCATATGATTTATTCGGAAGGACCTTCCT 725
 QY 181 LeuSerAspMetAlaMetGlyLysThrThrArgLysGlnIleValAsnLeuSerAsn 200
 Db 726 CTTAGTACATGCGCATGGGAGAGACACACAGGCGCATATGTCATTTGCTGTCCAT 785
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
 Db 786 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTAACTTCTGTGGGCAAGACCACTG 845

QY 221 GlnAlaIleAlaValThrAlaLeuThrPheGluIleGlyIleSerCysLeuAlaGly 240
 Db 846 CAGGCGATCGCATGATCCCTACTCTGATGAGATAGAAATATCGTCTCTGCGG 905
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 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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 QY 281 ThrGlyIleArgIleIleIysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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 QY 301 AsnLeuArgLysGluIleSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320
 Db 1086 AATTGAAAGAAAGAGATTTCCAAAGATTCGAGAGATTCCTGCTCAGGCGGATGAT 1145
 QY 321 LeuIleSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrVal 340
 Db 1146 TTGGCTTGTGTTTTCAGTGAAGCAAAATCATCGTTTGTGACCTTCAACCACTTACG 1205
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 Db 1206 CTCTCGGACATGTATCATACAGCCGCGTTCGTGGCAGATCACTGTATGGGCT 1265
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
 Db 1266 GTGGCGGTGAGGTATCCCTCTTCTCCCTCAGCATTTGAGAGGGGTGACAGAGCAATC 1325
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
 Db 1326 GTCAAGATCCAGAGATCCAACTTTTGTCTACTTGAAGATATCAAGGCAACCGT 1385
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 Db 1386 CAGCTGCGGTGATGTATTAAGATGATGATGATGATGATGATTTTACGCTTTTGGAT 1445
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 Db 1446 AAGGATCAGAGACCCCACTCAAGAGCCCTTCTTATCTGACAGCTGCGCAATTTG 1505
 QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
 Db 1506 TTAGCTGTGTGCGGCCCGTGGAGCAGAGAAATCATCACTGTAAAGTGTGCTCGG 1565
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
 Db 1566 GAATGGCCCAAGTCAAGGCGCTGCTAGCGTCAAGTGAAGATTTGCCATATGTGCTCAG 1625
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 QY 501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
 Db 1686 AAGGAACATATGAAAAAGTCAATAAGGCTTGCTGAAAAAGATTTACAGCTGTTG 1745
 QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyValLys 540
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 QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
 Db 1866 CCTCTCACTGACATGATGAGCGGAAGTTAGCAGACCTTGTTCGAACCTGTATTTGTCAA 1925
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Db 1926 ATTGTCAGAGAGATGACAAATTTAGACTCAGTCAGTGCAGTCAAAAGCTGCA 1985
Qy 601 SerGlnIleuLeuIleuLeuSapSgIyLySmeValIgluSgIyThrTyThrgluPhe 620
Db 1986 AGTCAGATTCGTATATTTGAAGATGTTAAATGCTCAGAGAGGCACTTACCTAGTTC 2045
Qy 621 LeuLySeserGlyIleAapPheGlySerLeuLeuLySapSngIgluSergIgluIn 640
Db 2046 CTAAATCTGTGTATAGATTTGGCTCCCTTTTAAAGAGATPAAATAGAGAAAGTGAACA 2105
Qy 641 PropIrovalProGlyIyThrProThrLeuAArgAnaArgThrPheSergIuserSerValITrp 660
Db 2106 CCTCAGATTCAGAGAACTCCACACTAAGAAATCGTACCTTCACAAAGCTTCGATTTG 2165
Qy 661 SerGlnIuserSerArgProSerLeuLySapSgIyAlaLeuGluSergInAspThrglu 680
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Qy 681 AsnValProvalThrLeuSergIgluIuAsnArgSergIgluLySValGlyPheGlnAla 700
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Qy 701 TyTyLSasntTyPheArgAlaGlyAlaHsITrPIleValPheIlePheLeuIleLeu 720
Db 2286 TATAAAGATTAATCTCAGAGCTGGTGTCTCAGTGAATGCTTCATTTCTTATTTCTCA 2345
Qy 721 AantThAlaAlaGlnValAlaTyValLeuGlnAspTrpTrpLeuSergTyTrpAlaAsn 740
Db 2346 AACACTGCAGCTCAGGTTGCTCTATGCTTCAAGATTTGGTGGCTTTCATACGGGCAAC 2405
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Qy 761 LeuAsnTrpTyLeuGlyIleTySergIyLeuThValAlaThrValLeuPheGlyIle 780
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QY 1321 PhegJurnrAlaLeu 1325
 DB 4145 TTCGAGACGACGACTG 4159
 RESULT 10
 US-09-439-313-536
 ; Sequence 536, Application US/09439313
 ; Patent No. 6329505
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
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 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Ranger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solt, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C9
 ; CURRENT APPLICATION NUMBER: US/09/439,313
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 536
 ; LENGTH: 6140
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (4535)
 ; OTHER INFORMATION: n=A,T,C or G
 ; US-09-439-313-536
 Alignment Scores:
 Pred. No.: 0 Length: 6140
 Score: 6600.50 Matches: 1300
 Percent Similarity: 97.0% Conservative: 0
 Best Local Similarity: 97.0% Mismatches: 0
 Query Match: 97.3% Indels: 40
 DB: 3 Gaps: 1
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 DB 295 TCAGGCTGCCAAGAACGCTCACAGCACCTTGAGAGAGAGTTGCAAGGGTCTGGGAT 354
 QY 66 LysGluValLeuAlaGlyAlaGluAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
 DB 355 AAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAAAGCTTTTAAACAAAGCAATCTA 414
 QY 86 LysCysTrrPlySerSerTrrLeuValLeuGlyIlePheThrLeuIleGluSerAla 105
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DB 595 CTCATTTGGCTAATAGCATCACTTATATTTTATACGTTACGTGCGGATGAGG 654
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 QY 206 AspGlnValThrValPheLeuHisPheLeuTrrAlaGlyProLeuGlnAlaIleAlaVal 225
 DB 775 GATCAGGTGACAGGTTCCTTACCTCCGTGGCAGAGCACATGACGAGCGATGCAAGT 834
 QY 226 ThrAlaLeuLeuTrrMetGluIleGlyTrrSerCysLeuAlaGlyMetAlaValLeuIle 245
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 DB 895 ATTCTCTGCCCCCTTGCAAAGCTGTTTGGAAAGTTTCTCATCATGAGAGATAAACT 954
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Oy 606 LeuysAspGlyLyAsnecValGlnuysGlyThrTyrgThrglnuPheLeuysSerGly11e 625
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QY 1290 ----- 1290
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QY 1291 -----ValIyrPheIleArgAsnTyrProHisIleGlyHisThrAspHisIle 1306
Db 4135 ACGCCAGCGCTGAGTATCTTCAAAAGAAATATCCACATATGGTCACTGACACCAT 4194
QY 1306 TValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
Db 4195 GGTTCAAACACTTCATCAATGACAGCCCTCGACCTTAATTTTGTGAGACGACATG 4252

RESULT 11

US-09-636-215-536

Sequence 536, Application US/09636215

Parent No. 6620922

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Mang, Aijun
APPLICANT: Skeiky, Yaser A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.4271C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(6140)
OTHER INFORMATION: n=A,T,C or G
US-09-636-215-536

Alignment Scores:

Pred. No.: 0 Length: 6140
Score: 6600.50 Matches: 1300
Percent Similarity: 97.04 Conservative: 0
Best Local Similarity: 97.04 Mismatches: 0
Query Match: 97.34 Indels: 40
DB: 3 Gaps: 1

US-09-976-858-42 (1-1325) x US-09-636-215-536 (1-6140)

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QY 46 SerValIleuProGluAspArgSerGlnHisLeuGlyGluIleuGlnGlyPheTrpAsp 65
Db 295 TCAGTGTGCGCCAGAGAGACCGCTCACAGCACCCTTGAGAGAGAGTTCCAGGGCTTCGGAT 354
QY 66 LysGluValIleuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
Db 355 AAAGAGTTTAAAGAGCTGAGAGATGACGACAGAGCCCTCTTTAAACAGAGCAATCATTA 414
QY 86 LysCysTyrTrpLysSerTyrLeuValIleuGlyIlePheThrLeuIleGluIleuSerAla 105
Db 415 AAGTCTTCTGGAATCTTATTTAGTTTGGAAATTTTACCTTATTAAGAGAAAGTGGC 474
QY 106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
Db 475 AAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTTGAATAATATGATCCC 534
QY 126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
Db 535 ATGATTTCTGTGGCTTTAAACACAGCGTACGCTATGCGCAGGTGCTGATTTTGGACG 594
QY 146 LeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
Db 595 CTCATTTTGGCTATATCTGATCATCATTAATTTTATACGTTCACTGTGCTGGATGAG 654
QY 166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
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QY 206 AspGlnValThrValPheLeuHisIlePheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
Db 775 GATCAGGTGACAGTGTCTTACATCTTCTGTGGGAGAGACCATGACGAGATCCAGTG 834
QY 226 ThrAlaLeuLeuTrpMetGluIleGlyLysSerCysLeuAlaGlyMetAlaValLeuIle 245
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QY 246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
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QY 266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
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QY 366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
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QY 386 IleGlnThrPheLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405

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 QY 586 IILETRTILEUVALTHRTISGLINLEUGINTRYRLEUVALALASERGINILEUUILE 605
 Db 1915 ATCACAAATTTTATGATCATCATAGTTGACAGTACTCAAGCTGCAAGTCAAGATTCGATA 1974
 QY 606 LEULYASPARGLYMETVALGILNYSGLYTHRTRYRGLUPHEULYSSERGLYILE 625
 Db 1975 TTGAAAGATGTAAATGTGTGCAAGAGGGACTTACATGAGTTCCTTAAATCTGGTATA 2034
 QY 626 AAPHEGLYSERLEULEULYSLYSASPANGILNUSERGLINGINPROVALPROGLY 645
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 QY 646 THRPROTHLEUARGASPARGTHRPHESERGLUSERSERVALTRYSERGININUSER 665
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 QY 666 ACTPROSELEULYASPARGLYALALEUGLUSERGINASPTHRGLUNASVALPROVALTHR 685
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 QY 686 LEUSERGLINLUSANRSGERGLYLYSVALGILYPHEGINALATRYLYSANTRYPHE 705
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 Db 2275 AAGAGCTGTGTCTCAGATGTGTCTTCAATTTCTTAATCTCTTAACACTGACGTCTAG 2334
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Db 2395 AATGTCACTGTAAATGAGAGGAAATGTAAACCGAAGACTAGATCTTAAGCTGTACTTA 2454
 QY 766 GILYLYSERGLYLEUTHRVALALATHRVALLLEUPHEGLYILEALARGSERLEUEN 785
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 Db 2635 TCCAAAGACATTTGACACTTGGATGATTTGCTGCGCGCTGAGAGTTTATGATTTCAATCCAG 2694
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 QY 1066 LYSERGLINLUSYVALGILYRILEVALGILYARGTRNGLYVALGILYLSERSESERLEUILE 1085
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 DB 3535 TTGTTCACTGGAGCAATGGAGAAAACCTGGATCCCTTTAAAGAGACAGGATGAGGA 3594
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 DB 3655 ATGGATTAAGTAATGGAGAAATCAGGATCAATTTAGTTGGACAAAGACACAGTG 3714
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 QY 1206 AsnValAspProArgThrAspGluLeuIleGlnLysValLeuArgGluLysPheAlaHis 1225
 DB 3775 AATGTGATCCAGAACTGATGATTAATCAAAAATAATCCGGAGAAATTTGCCAC 3834
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 DB 3835 TGCACTGCTACCATTCGACACAGATTGAACCATATTGACACAGCAAGATTAATG 3894
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 DB 4015 GAACAGCAAAACAGAGATGGGTTTACCATGTTGGCCAGCTGGTCAAACTCTGA 4074
 QY 1290 ----- 1290
 DB 4075 CCTCAAGTATCCACCTGCTGGCTCCCAAACTGCTGAGATTACAGGTGAGCCACC 4134
 QY 1291 -----ValTyPheLysArgAsnTyPProHisIleGlyHisThrAspHisMet 1306
 DB 4135 AGCCCAAGCTGATGATTAATCTTCAAAAGAAATTAATCACTATTTGTCACACTGACCACT 4194
 QY 1306 ValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
 DB 4195 GGTACAAACACTTCCAATGACAGCCCTGCACTTAATTTTGGAGACGACACTG 4252
 RESULT 12
 US-09-685-166A-536
 ; Sequence 536, Application US/09685166A
 ; Patent No. 6630305
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
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 ; APPLICANT: Retter, Marc W.
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 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yahir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C21
 ; CURRENT APPLICATION NUMBER: US/09/685,166A
 ; CURRENT FILING DATE: 2000-10-10
 ; NUMBER OF SEQ ID NOS: 898
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 536
 ; LENGTH: 6140
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(6140)
 ; OTHER INFORMATION: n=A,T,C or G
 ; US-09-685-166A-536
 Alignment Scores:
 Pred. No.: 0 Length: 6140
 Score: 6600.50 Matches: 1300
 Percent Similarity: 97.04 Conservative: 0
 Best Local Similarity: 97.04 Mismatches: 0
 Query Match: 97.38 Indels: 40
 DS: 3 Gaps: 1
 US-09-976-858-42 (1-1325) x US-09-685-166A-536 (1-6140)
 QY 26 TTPLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluAspAspMetTyr 45
 DB 235 TGGCTCAATCCCTGTTTAAATGGCCATTAACGGAATTAAGAGAAAGATATATAT 294
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 DB 475 AAAGTAATCCAGCCCATATTTTGGGAAAATTAATTAATTTGAAAATTAATATCC 534
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 QY 186 MetGlyTyPThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
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 QY 246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerTyPThr 265
 DB 895 ATTCTCGCCCTTGCAAGCTGTTTGGAAATGTTCTCATCTACATGAGAGATAAACT 954

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QY 586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
DB 1915 ATCACAAATTTAGTCACTCATCAGTTGCACTACCTCAAGCTCAAGTCAAGATTCGATA 1974
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DB 1975 TTAAAGATGTAAATGTGCGAAGGGGACTTACCTGAGTTCCATAAATCTGGGATA 2034
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RESULT 13
 US-09-679-426-536
 / Sequence 536, Application US/09679426
 / Patent No. 6759515
 / GENERAL INFORMATION:
 / APPLICANT: Xu, Jianshun
 / APPLICANT: Dillon, Davin C.
 / APPLICANT: Mitchem, Jennifer L.
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 / APPLICANT: Jiang, Yuqi
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Ranger, Gary R.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedick, Thomas S.
 / APPLICANT: Carter, Darlick
 / APPLICANT: Li, Samuel
 / APPLICANT: Wang, Aijun
 / APPLICANT: Skeiky, Yasir A.W.
 / APPLICANT: Hepler, William
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 / TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 / FILE REFERENCE: 210121.427C20
 / CURRENT APPLICATION NUMBER: US/09/679, 426
 / CURRENT FILING DATE: 2000-10-02
 / NUMBER OF SEQ ID NOS: 895
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 536
 / LENGTH: 6140
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / LOCATION: (1) ..(6140)
 / OTHER INFORMATION: n-A, T, C or G
 US-09-679-426-536
 Alignment Scores:
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 Score: 6600.50 Matches: 1300
 Percent Similarity: 97.0% Conservative: 0
 Best Local Similarity: 97.0% Mismatches: 0
 Query Match: 97.3% Indels: 40
 DB: 3 Gaps: 1
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QY 166 LeuArgValAlaMetCysH1Met1IeTyArgValAlaLeuArgLeuSerAsnMetAla 185
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RESULT 14

US-09-759-143-536
Sequence 536, Application US/09759143
Patent No. 6800746

GENERAL INFORMATION:

```

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(6140)
OTHER INFORMATION: n=A,T,C or G
US-09-759-143-536

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Alignment Scores:

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Pred. No.: 0 Length: 6140
Score: 6600.50 Matches: 1300
Percent Similarity: 97.08 Conservative: 0
Beet Local Similarity: 97.08 Mismatches: 0
Query Match: 97.38 Indels: 40
DB: 3 Gaps: 1

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US-09-976-858-42 (1-1325) x US-09-759-143-536 (1-6140)

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 QY 126 MetAaspSerValAlaLeuAasnThraIaTYraIaTYraIaThrValLeuThrPheCysThr 145
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 QY 146 LeuIleLeuAlaIleLeuHISLeuTYrPheTYrHISValGIuCysAlaIleMetArg 165
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 QY 166 LeuAArgValAlaMetCysHISMetIleTYrAArgValaLeuAArgLeuSerAaspMetAla 185
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 US-09-651-236-536
 ; Sequence 536, Application US/09651236
 ; Patent No. 6818751
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.42718C18
;; CURRENT APPLICATION NUMBER: US/09/651,236
;; CURRENT FILING DATE: 2000-08-29
;; NUMBER OF SEQ ID NOS: 865
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 536
;; LENGTH: 6140
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(6140)
;; OTHER INFORMATION: n=A,T,C or G
US-09-651-236-536

Alignment Scores:

Pred. No.:	0	Length:	6140
Score:	6600.50	Matches:	1300
Percent Similarity:	97.0%	Conservative:	0
Best Local Similarity:	97.0%	Mismatches:	0
Query Match:	97.3%	Indels:	40
DB:	3	Gaps:	1

US-09-976-858-42 (1-1325) x US-09-651-236-536 (1-6140)

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 Db 2455 GGAATTTATTCAGTTTAACTGATGCTACGTTCTTTTGGCATGCAAGATCTGATATG 2514
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 QY 926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
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Search completed: March 14, 2006, 13:53:46
Job time : 763 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 14, 2006, 15:52:06 ; Search time 1653 Seconds
(without alignments)
1849.467 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6767

Sequence: 1 MLPVQVEKRPPLDANICS.....MTNTSNGPSTLTIFETAL 1325

Scoring table:

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Ygapop 10.0, Ygapext 0.5	
Fgapop 6.0, Fgapext 7.0	
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Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA New -OPMT=fastcap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6787	100.0	5716	12 US-11-124-367A-149	Sequence 149, App
2	6779	99.9	4231	7 US-10-329-258-9	Sequence 9, Appl1
3	6760	99.6	6082	12 US-11-234-786-535	Sequence 535, App
4	6686	98.5	5875	12 US-11-091-883-414	Sequence 414, App

5	6600.5	97.3	6140	12 US-11-234-786-536	Sequence 536, App
6	3310.5	48.8	2143	12 US-11-124-367A-150	Sequence 150, App
7	3262	48.1	2256	12 US-11-124-367A-148	Sequence 148, App
8	2285.5	33.7	5011	7 US-10-825-585-35	Sequence 35, Appl1
9	2285.5	33.7	5011	7 US-11-045-578-3	Sequence 3, Appl1
10	2263	33.3	4587	12 US-11-045-578-2	Sequence 2, Appl1
11	2235	32.9	4599	12 US-11-045-578-1	Sequence 1, Appl1
12	2227	32.8	4551	7 US-10-932-182A-484	Sequence 484, App
13	2227	32.8	4551	7 US-10-932-182A-484	Sequence 484, App
14	2201	32.4	4954	12 US-11-136-527-2145	Sequence 2145, App
15	2174	32.0	5189	12 US-11-136-527-475	Sequence 475, App
16	2087	30.7	6129	7 US-10-501-035-124	Sequence 124, App
17	2087	30.7	6129	7 US-11-206-139-1	Sequence 1, Appl1
18	2087	30.7	6129	12 US-11-127-832-24	Sequence 24, Appl1
19	2052	30.2	5762	12 US-11-136-527-489	Sequence 489, App
20	2037.5	30.0	5139	12 US-11-132-864-47	Sequence 47, Appl1
21	2037.5	30.0	5143	12 US-11-054-168B-20	Sequence 20, Appl1
22	1988	29.3	3918	9 US-11-096-568A-29801	Sequence 29801, A
23	1887.5	27.8	4434	7 US-10-932-182A-76875	Sequence 76875, A
24	1887.5	27.8	4434	7 US-10-932-182A-76875	Sequence 76875, A
25	1867	27.5	4986	7 US-10-932-182A-1658	Sequence 1658, App
26	1867	27.5	4986	7 US-10-932-182A-1658	Sequence 1658, App
27	1843.5	27.2	4686	7 US-10-932-182A-3096	Sequence 3096, App
28	1843.5	27.2	4686	7 US-10-932-182A-3096	Sequence 3096, App
29	1825	26.9	4680	7 US-10-932-182A-191051	Sequence 191051, A
30	1825	26.9	4680	7 US-10-932-182A-191051	Sequence 191051, A
31	1802.5	26.6	5792	12 US-11-136-527-2846	Sequence 2846, App
32	1760	25.9	4826	12 US-11-030-439-23	Sequence 23, Appl1
33	1748	25.8	4977	12 US-11-090-439-25	Sequence 25, Appl1
34	1661	24.5	3357	7 US-10-932-182A-80104	Sequence 80104, A
35	1661	24.5	3357	7 US-10-932-182A-80104	Sequence 80104, A
36	1650.5	24.3	4999	8 US-10-995-561-10	Sequence 10, Appl1
37	1649	24.3	5064	8 US-10-995-561-9	Sequence 9, Appl1
38	1557.5	22.9	3910	8 US-10-995-561-451	Sequence 451, App
39	1543.5	22.7	2682	7 US-10-932-182A-5556	Sequence 5556, App
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ALIGNMENTS

RESULT 1
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; Sequence 149, Application US/11124367A
; Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 5716
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-124-367A-149
Alignment Scores: 0 Length: 5716
Pred. No.: 0

Score: 6787.00 Matches: 1325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0
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DB 61 CGGCTGTTCTTCTGGTGGCTCAATCCCTGTTAAATTGGCCATTAACGAGATTAAAG 120
QY 41 GluAspAspMetCysSerValLeuProGluAspArgSerGlnHisLeuGlyGlyGluLeu 60
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(4093)
; OTHER INFORMATION:
US-10-329-258-9

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DB      476 GAAATATATGATCCCATGGATTTCTGTGCTTGAACACAGCGTAGCCCTATGCGACGGTG 535
QY      141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTrpPheTrpHisValGln 160
DB      536 CTGACCTTTTGCACGCTCATTTTGGCTATACGACATCACTTATATTTTATCACGTTGAG 595
QY      161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTrpArgLysAlaLeuArg 180
DB      596 TGTGTGGGATAGAGTTTACGAGTAGCCATGTCCATATGATTTATTCGAAAGCACCTTCGT 655
QY      181 LeuSerAsnMetAlaMetGlyLysThrTrpThrGlnIleValAsnLeuSerAsn 200
DB      656 CTTAGTAACATGACCGGAGGAGAACACACACGAGCAATGATCATCTGCTGTCATAT 715
QY      201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
DB      716 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTTCACCTTCCTGGGACAGGACCACTG 775
QY      221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
DB      776 CAGGCATGCGAGTGACTGCCCTACTCTGATGAGATAGAAATATCGTCTTGCTGGG 835
QY      241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
DB      836 ATGGAGATTCTATCATCTCTCCGCTTGCAAAAGCTGTTTGGGAAAGTTGTTCTCATCA 895
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QY      281 ThrGlyIleArgIleIleLysMetTrpAlaTrpGluLysSerPheSerAsnLeuIleThr 300
DB      956 ACTGATTAAGGATTAATTAATAATGTACCCCTGGGAAAAGTCAATTTTCAAACTTATTAC 1015
QY      301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320
DB      1016 AATTGGAAGAAAGAGGATTTCCAAAGATTCGAGAACTTCCTGCTCAGGGGGATGATAT 1075
QY      321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTrpVal 340
DB      1076 TTGGCTGTGTTTTCAGTGACAGCAAAATCACTCGGTGTGACCTTACCACTTACGATG 1135
QY      341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTrpGlyVal 360
DB      1136 CTCTCGGACAGTGATACAGCCAGCCGCTGTTTCGTGGACGTACCTGTATGGGCT 1195
QY      361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
DB      1196 GTGGCGCTGACGGTTAACCTCTTCTCCCTCAGCATTTGAGAGGGGTGTCAGAGCAATC 1255
QY      381 ValSerIleArgArgIleGlnThrPheLeuLeuAspGluIleSerGlnArgAsnArg 400
DB      1256 GTCAAGCATCCGAAAGATCAGACCTTTTGGCTACTGTATGATATCAAGGCAACCTGT 1315
QY      401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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QY      421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
DB      1376 AAGCATGACAGAACCCCAACTCTACAGGCCCTTCTTACGTGACAGCTGGCGAATTG 1435
QY      441 LeuAlaValAlaGlyProValGlyValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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QY      461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTrpValSerGln 480
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QY      501 LysGluArgTrpGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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QY      521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
DB      1676 GAGGATGTGATCTACCTGTGATAGAGATCGGGGAAACCAAGCTGATGAGGGGAGAA 1735
QY      541 AlaArgValAsnLeuAlaArgAlaValTrpGlnAspAlaAspIleTrpLeuLeuAspAsp 560
DB      1736 GCGCGGATTAACCTTGCAGAGCACTGTATCAAGATGCTGACATATCTCTCGACCAT 1795
QY      561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlnLeuCysIleCysGln 580
DB      1796 CCTTCAGTGACGTAGATCGGGAATGTAGACACACTTGTTCGAACCTGTGATTTGTCAA 1855
QY      581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTrpLeuLysAlaAla 600
DB      1856 AATTTCATGAGAAATATCAAAATTTAGTCACTCACTGACGTGCACTTAACTGCA 1915
QY      601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTrpThrGluPhe 620
DB      1916 ACTCAGATTCTCATTTTGAAGATGTATAAATGTGTGACGAAGGAGCACTTACACTAGTTC 1975
QY      621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGlnSerGlnGln 640
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 Qy 681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyValValGlyPheGlnAla 700
 Db 2156 AATGCCCCAGTTACCTATACAGAGAGAACCTTCTGAAAGAAAGTTGTTTCAGGCG 2215
 Qy 701 TyrLeuAsnThrPheArgAlaGlyAlaHisTyrPheLeuPheLeuLeuLeu 720
 Db 2216 TATAAGAAATTAATCTCAGAGCTGCTGCTCAGATTTGCTCATTTTCTTATCTCCTA 2275
 Qy 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrPheLeuSerTyrThrAlaAsn 740
 Db 2276 AACACTGACGCTCAGAGTGGCTTAGTGTCTCAAGATGGTGGCTTTCATACCTGGCGAAC 2335
 Qy 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGluLysLeuAsp 760
 Db 2336 AACCAAGATATCTAAATCTCACTGTAATGAGAGAGAAATCTAACCGAGAACTAGAT 2395
 Qy 761 LeuAsnThrTyrLeuGlyLysTyrSerGlyLeuThrValAlaThrValLeuPheGlyLe 780
 Db 2396 CTAACTGGTACTTAGAAATTTATTCAGGTTTAACGTAGTACCGTCTTTTGGCATA 2455
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 Db 2576 ATTTTAAATCGTTTCTCCAAAGACATGGACACTTGATGATTTGGTCCGCTGACGTTT 2635
 Qy 841 LeuAspPheLeuGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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 Db 3236 ATTAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTCTGTACTGAAGCAT 3295
 Qy 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyLysValGlyArgThrGlyAlaGly 1080
 Db 3296 CTGACAGACCTATTAAATCAAGAAAGGTGGCATTTGGAGAAAGACCGAGCTGGA 3355
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 Qy 1101 AspLysLysLeuThrThrGluLysLysLysLysLysLysLysLysLysLysLysLysLys 1120
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 Db 3476 CCTCAGAACTGTTTGTTCATCTGGAACATAGAGAAACCTGGAATCCCTTTAAGAG 3535
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 Db 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuLysLysLysLysLys 1220
 Qy 3716 GATGAAGGAGCGCAATGTGATTCAGAACTGATGCTTATACAAAAAAATCCGG 3775
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 Qy 3956 GCCGCTGCCCTCAGTGAAGACGCAAAACAGATATCTTCAAAAGAAATTTATCCACATTT 4015
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RESULT 3
 US-11-234-786-535
 ; Sequence 535, Application US/11234786

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Publication No. US20060024301A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
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APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
FILE REFERENCE: 210121.427C31
CURRENT APPLICATION NUMBER: US/11/234,786
PRIOR APPLICATION NUMBER: US 09/568,857
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 09/536,857
PRIOR FILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: US 09/483,672
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 09/439,313
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/352,616
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: US 09/288,946
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/232,149
PRIOR FILING DATE: 1999-01-15
PRIOR APPLICATION NUMBER: US 09/159,812
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 09/115,453
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR FILING DATE: 1998-02-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 701
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-11-234-786-535

Alignment Scores:
Pred. No.: 0 Length: 6082
Score: 6760.00 Matches: 1324
Percent Similarity: 99.9% Conservative: 0
Best Local Similarity: 99.9% Mismatches: 1
Query Match: 99.6% Indels: 1
DB: 12 Gaps: 0

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DB 186 ATGCTGCCCGTGTACCAAGAGGTGAAGCCCAACCGCTGCAAGACCGAACTTCTGCTCA 245
QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgLeuGln 40
DB 246 CCGGTGTTCTTCTGGGTGCTCAATCCCTGTTTAAATTGGCCATPAAACGAGATTAGAG 305
QY 41 GluAspAsnMetLysSerValLeuProGluAspArgSerGlnHisLeuGlyValGluLeu 60
DB 306 GAAAGATGATATGTATTCAAGTGTGCTGCAGAAACCGCTCAAGACCTTGAGAGAGTTGG 365
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QY 61 GlnGlyPheTrpAspArgLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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QY 81 ThrArgAlaIleIleLysCysEtyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
DB 426 ACAAGAGATCATTAAGTGTATCTGGAATCTTATTTAGTTTGGAAATTTTACGTGA 485
QY 101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
DB 486 ATTGAGGAAGTCCAAAGTATATCCAGCCATATTTTGGGAAAAATTAATTAATTAATTT 545
QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140
DB 546 GAAATATTGATCCCATGATTCGTGCTTGAACACAGGCTACGCTATGCCACGGTGG 605
QY 141 LeuThrPheCysTrpTrpLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
DB 606 CTGACTTTTTCAGCGCTCATTTTGGCTATCTGATCTCATCTTAATTTTATCAGTTGAG 665
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
DB 666 TGTGCTGGAGTAGAGTTTACAGTAGTGCATGTCATATGATTTATCGGAAGGCACTTCGT 725
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrGlyGlnIleValAsnLeuSerAsn 200
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QY 201 AspValaLeuLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
DB 786 GATGGAACAAATTGATCAGGTGACAGTGTCTTCACTTCTGCTGGGACAGACCATG 845
QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgTrpMetAsnGluValIle 280
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DB 1386 CAGTCCCGTCAAGATGTAAAGATGTGATGTGATGTCAGATTTTACTGCTTTTGGGAT 1445
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QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGlnLeu 440
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DB 1506 TTAGCTGTGGTGGCCCCGCTGGGACAGAGGAGTCATCTGTAAAGTCCCTGCTGGG 1565
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DB 1566 GAATGGGCCCAAGTCAGCGCTGGTCAAGCTGTCAAGAAATTGCTATGTGCTCAG 1625
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DB 1866 CCTCAGTGCAGTATGATGCGGAGATTAGCAGACACTGTTGAACTGTGATTTGTGCA 1925
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DB 1926 ATTTTGATGTAGAAATCACAATTTTAGTACTCATCAGTTCAGTCACTCAAACTGCA 1985
QY 601 SerGlnIleLeuIleLeuYsaAspGlyLeuMetValGlnLeuGlyThrTyrThrGlnPhe 620
DB 1986 AGTCGATTTCTGATATTGAAAGATGTAAATGTGTGCAGAGGGACCTTACCTAGTTC 2045
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DB 2766 ATTCCTTGGATCGCAATACCTTGGTTCCTCTGGAAATCATTTTCTTCTGGCGCA 2825
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DB 2946 GAGAGTGTCAAGAACTGTTGATGACACACAGATTTTACATTCAGAGCTGTGTTCTTGG 3005
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DB 3006 TTTTGAACAGCTCCGCTGGTGCCTGCTGAGTGAAGCATGTGTCATGTTTGTTC 3065
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DB 3066 ATCAATCGTTGCTTGGGTCTCTGATCTGGCAAAAATCTGGAGTCCGGGAGGTTGCT 3125
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000
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QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLeuHis 1060
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QY 1061 LeuThrAlaLeuIleYsaSerGlnGlnLeuValGlyIleValGlnArgThrGlnValGly 1080
DB 3366 CTGACAGACATTAATTAATCAAGAAAGGTTGGCATTTGGGAAAGAACCGAGACTGGA 3425
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGlnProGlnGlyLeuIleTyrPile 1100
DB 3426 AAAAGTCTCCATCTCACTGACCTTTTATGATGTGTCAAGAACCGAAAGTAAATTTGAAAT 3485
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DB 3546 CCTCAGAACTGTTTGTTCATCTGGAACAAATGAGAAACCTGGAATCCCTTTATATAG 3605
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RESULT 4
US-11-091-883-414
; Sequence 414, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIFF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 414
; LENGTH: 5875
; TYPE: DNA
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; NAME/KEY: modified base
; LOCATION: (5689)..(5689)
; OTHER INFORMATION: a, c, g, or t
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US-11-091-883-414

Alignment Scores:

Pred. No.:	0	Length:	5875
Score:	6686.00	Matches:	1315
Percent Similarity:	99.14	Conservative:	1
Best Local Similarity:	99.08	Mismatches:	9
Query Match:	98.54	Indels:	3
DB:	12	Gaps:	0

US-09-976-858-42 (1-1325) x US-11-091-883-414 (1-5875)

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QY 21 ArgValIlePhePheTrpLeuAsnProLeuPheIySIIeGlyHIleIySArgTrgLeuGlu 40
DB 176 CCGGTTCTCTGGGCTCAATCCCTGTTAAATGGCCATMAACGGAGATTAGAG 235
QY 41 GluAspAspMetTySerValIleuProGluAspArgSerGlnHIleuGlyGluLeu 60
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QY 61 GInGlyPheTrpAspLySgluValIleuArgAlaGluAsnAspAlaGlnLySProSerLeu 80
DB 296 CAAGGCTTCTGGATTAAGAAAGTTTAAAGACTGAGAAATGACGACAGAGAGCTTCTTTA 355
QY 81 ThrArgAlaIleIleIySeySerTyTrpLySeryTyLeuValIleuGlyIlePheTrileu 100
DB 356 ACAAGAGCAATCATMAAGTTTACGAAATCTTATTAAATTTGGAAATTTTACGTTA 415
QY 101 IlegluSerAlaIyValIleGlnProIlePheLeuGlyIySIIeIleAsnTyPhe 120
DB 416 ATTGAGAAAGGCCAAAGTATCCAGCCCATATTTTGGAAAAATTTATTAATTAATTTT 475
QY 121 GluAsnTyAspProMetAspSerValAlaIleuAsnThrAlaTyAlaThrVal 140
DB 476 GAAATTTATGATCCCATGATTCCTGGCTTTGAAACAGCGGTACGCCATGCCAGG 535
QY 141 LeuTrPheCySThrLeuIleleuAlaIleleuHIleuHIleuTyPheTyRHIleValGln 160
DB 536 CTGACTTTTGGACCTCATTTTGGCTATACGCTATCATTAATTTTATCATCCTGAG 595
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHISmetIleTyArgLySAlaLeuArg 180
DB 596 TGTGCTGGAGTGAAGGTTCAGAGTACCATGTGCCATATGATTTATCGAAGGACCTTGT 655
QY 181 LeuSerAsnMetAlaMetGlyIySThrThrThrglyGlnIleValAsnLeuSerAsn 200
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QY 201 AspValIleuLySAspPheGlnValIleValIlePheIleuHIlePheLeuTrpAlaGlyProLeu 220
DB 716 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGGAGACACATG 775
QY 221 GlnAlaIleAlaValIleThrAlaLeuLeuTrpMetGlnIleGlyIleSerCysLeuAlaGly 240
DB 776 CAGGAGATCGAGTACCTGCTACTGTAGATGAGATGAGAAATTCGTGCTTGTG 835
QY 241 MetAlaValIleuIleIleuLeuProLeuGlnSerCysPheGlyIySLeuPheSerSer 260
DB 836 ATGGCAGTTCTTAATCATTTCTCTGCTTTCGAAAGCTGTTTGGAAATGTGTTCTCAACA 895
QY 261 LeuArgSerLySThrAlaThrPheThrAspAlaArgIleArgThyMetAsnGluValIle 280
DB 896 CTGAGAGATTAACAACGCAACTTTCAGCGATGCGAGATCAGAGACATCAATGAAGTTTATA 955
QY 281 ThrGlyIleArgIleIleIySmetTyAlaTrpGluLySserPheSerAsnLeuIleThr 300
DB 956 ACTGATTAAGAGATATAAATGTACGCTGNGNNAAGCANNNTCCNNNNNNNTTACC 1015
QY 301 AsnLeuArgLySlySgluIleSerLySIIeLeuArgSerSerCysLeuArgGlyMetAsn 320
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DB 1076 TTGGCTGTGTTTTCAGTGAAGCAAAATCATGTGTTGTGACCTTCAACCACTTACGTG 1135
QY 341 LeuLeuGlySerValIleThrAlaSerArgValIlePheAlaIleValIleThrLeuTyRgIyAla 360
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RESULT 5

US-11-234-786-536

; Sequence 536, Application US/11234786

; Publication No. US20060024301A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yugu

; APPLICANT: Reed, Steven G.

; APPLICANT: Kloe, Michael D.

```

APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yael A.
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
FILE OF INVENTION: POLYPEPTIDES THEREOF
FILE REFERENCE: 210121.427C31
CURRENT FILING DATE: 2005-09-23
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 701
SOFTWARE: Paetseq for Windows Version 3.0
SEQ ID NO 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(6140)
OTHER INFORMATION: n=A,T,C or G
US-11-234-786-536

Alignment Scores:
Pred. No.: 0 Length: 6140
Score: 6600.50 Matches: 1300
Percent Similarity: 97.04 Conservative: 0
Best Local Similarity: 97.04 Mismatches: 0
Query Match: 97.34 Indels: 40
Gaps: 1
DB: 12

US-09-976-858-42 (1-1325) x US-11-234-786-536 (1-6140)
QY 26 TTPLEUAENPROLEUHPHELYSILEGLYHSATGATGLeuGluGluAspAspMetTyr 45
DB 235 TGGCTCAATCCCTTGTAAATGGCCATAACGAGATTAGAGAGATGATATGTAT 294
QY 46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheThrPhe 65
DB 295 TCAGTGTGCGCCAGAGACCGCTCACAGCCCTTGGAGAGAGATTGCAAGGTTTGGGAT 354
QY 66 LysGluValLeuArgAlaGluAspAlaGlnLysProSerLeuThrArgAlaLeuLeu 85
DB 355 AAAAGAGTTTAAAGCTGAGATGACGACAGAGGCTTTTAAACAAGACATCATCA 414
QY 86 LysGlyTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
DB 415 AAGGTCTACTGGAATCTTATTAGTTTGGGAATTTTACCTTAATGAGAGAAAGTGCC 474

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QY 106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
DB 475 AAAGTATCCAGCCCATATTTTGGGAAAATATATATATATTTGAAAATATATATCC 534
QY 126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
DB 535 ATGATCTCTGTGGCTTTGAACACAGCGCTATGCGACCGTCTGACCTTTTGGACG 594
QY 146 LeuIleLeuAlaIleLeuHisHisIleuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
DB 595 CTCATTTTGGCTATATCTGCATCATCTTAATTTTATACAGTTCACTGTGCTGGATGAGG 654
QY 166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
DB 655 TTACAGATGAGCATGTGCTCATATGATTTATATGGAAGGACCTTCCTTATGTAACATGCC 714
QY 186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
DB 715 ATGGGAAGACAAACACAGGCCAGATGATCATCTGTCTCCATGATGTGAAACAAGTTT 774
QY 206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
DB 775 GATCAGGTGACAGTGTGTTTACACTTCTGTGGCAGAGACCATGACAGCCATCCAGTG 834
QY 226 ThrAlaLeuLeuTrpMetGlnIleGlyLysSerCysLeuAlaGlyMetAlaValLeuIle 245
DB 835 ACTGCCCTACTCTGATGATGAGATGAGATATCTGCTTGTGGATGGCACTTCTATC 894
QY 246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
DB 895 ATTCCTCGCCCTTCAAAAGCTGTTTGGAAAGTTGTTCTCATCTACAGAGAGTAAACT 954
QY 266 AlaThrPheThrAspAlaArgIleArgThrMetLeuGlnValIleThrGlyIleArgIle 285
DB 955, GCACCTTTCAGGAGCCAGATCGACGACATGATGATGATTAATGATTAAGGATA 1014
QY 286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
DB 1015 ATTAATAATGATCGCTGGGAAAAGTCAATTTTCAATCTTATTAACATTTGGAAGAAG 1074
QY 306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
DB 1075 GAGATTTCCAAAGATCTGAGAAGTTCCTGCTCAGGGGATGAAATTTGGCTCGTTTTC 1134
QY 326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
DB 1135 AGTGCACAGCAAAATCATGTGTGTGTGACCTTACACACTACGTCTCTCGGAGTGTG 1194
QY 346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
DB 1195 ATCACAGCGACCGCGGTGTGTGTGTGACAGTGTATGAGGCTGTGTGCGCTGACGGTT 1254
QY 366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
DB 1255 ACCCTCTTCTCCCTCAGCCATTCAGAGGGGTGTCAGAGGCAATGTCAGATCCGAGA 1314
QY 386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerPhe 405
DB 1315 ATCCAGACCTTTTGTCTCTCTGATGAGATATCACGCCCAACCGTCACGTGCGTCAAGT 1374
QY 406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGlnThr 425
DB 1375 GGTAAAGATGTGTGATGTGATGATTTTACTGCTTTTGGATTAAGGATCAAGAGACC 1434
QY 426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValGly 445
DB 1435 CCAACTTACAAAGGCTTTCTCTTACTGTGACAGCTGCGAATTTTGTAGCTGTGCTCGC 1494
QY 446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
DB 1495 CCGGTGGAGAGAGGAAATCATCTGTTAAGTGTGCTGTGGGAAATTTGGCCCAAGT 1554
QY 466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485

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Db 1555 CACGGGCTGCTCAGCGTCATGGAAGAAATTCCTATGCTCTCACAGCCCTGGGCTGTTCC 1614
 QY SerGIYThrLeuArgSerAsnIleLeuPheGIYLYSLYSYrGLuYleuGIYArgTYrGLu 505
 Db 1615 TCGGGAACCTGAGAGCTAATATTTATTTGGGAAAGAAATACGAAAGGAACGATATGAA 1674
 QY LysValIleIeYsaIaCySaIaLeuYsaIeLeuGIYLeuLeuGIYAspGIYAspLeu 525
 Db 1675 AAAGCATPAAAGGCTTGCTGCTCGAAAAGATTTACAGCTGTGGAGGATGGTATCTCG 1734
 QY ThrValIleIeGIYAspArgGIYThrThrLeuSerGIYGIYGIYLeuYalAArgValAsnLeu 545
 Db 1735 ACTGTGAATGAGAGATCGGGGAAACAACGCTGAGTGGAGGGCAGAAAGCAACGGGTAAACCTT 1794
 QY AlaArgAlaValIYrGLuAspAlaAspIleIYrLeuLeuAspAspProLeuSerAlaVal 565
 Db 1795 GCAAGAGCATGTATCAAGATGCTGACATCTATCTCTGGACGATCTCTCACTGCACTGA 1854
 QY AspAlaGIYValIseArGIHleuPheGIYLeuCySileCySGLnIleLeuHleGIYLYS 585
 Db 1855 GATCGGGAAGTTAGCAGACACTTGTTGCACTGTGATTTGTCAAAATTTTGCATGAGAAG 1914
 QY IleThrIleIeValIleThrHleGIYLeuGIYrLYrLeuYalAAspSerGIYIleIeLeu 605
 Db 1915 ATCACAAATTTTAAAGTACATCATGATTCAGTACCTCAAGCTGCAAGCTCAGATTCGATA 1974
 QY LeuLYsaAspGIYLYMeCYValGIYnYsGIYrLYrLYrGLuPheLeuYsSerGIYIle 625
 Db 1975 TTGAAGATGTGTAAGATGTGCAAGAGGGGACTTACATGAGTTCTCTAAATCTGGTATA 2034
 QY AspPheGIYSerLeuLeuLYsaAspAsnGIYLeuGIYnYrProValIProGIY 645
 Db 2035 GATTTTGCTCCCTTTTAAAGAGATATAGAAAGTAAACAACCTCCATGTTCCAGGA 2094
 QY ThrProThrLeuArgAsnArgThrPheSerGIYLeuSerValITPserGIYnYnIseSer 665
 Db 2095 ACTCCACACTAAGGATGCTACTCTCAGAGCTTCGGTGTGGCTCAACAACCTTCT 2154
 QY ArgProSerLeuLYsaAspGIYAlaLeuGIYnYrAspThrGLuAsnValIProValIThr 685
 Db 2155 AACCTCTCTTAAAGATGTGCTCTGAGAGCCAGATACAGAGATGTCCAGTTACA 2214
 QY LeuSerGIYGLuAsnArgSerGIYLYrLYrValIleGIYPheGIYAlaTYrLYsaAsnTYrPhe 705
 Db 2215 CTATCAGAGAGAACCGTTCTGAGAGAAAGTTGGTTTTCAAGCCATTAAGAAATTAATCTTC 2274
 QY ArgAlaGIYAlaHleIleThrIleValIlePheIlePheLeuIleLeuLeuAsnThrAlaIleGIY 725
 Db 2275 AAGAGCTGGCTCAGCTGAGATGTCTTCATTTCTCTTAATCTCTAAACAACCTCAGCTCAG 2334
 QY ValAlaTYrValIleLeuGIYnYrTPTrLeuSerTYrTPTrAlaAsnLYsGIYnYrSerLeu 745
 Db 2335 GTTGCTGATGTGCTTCAAGATGTGGTGGCTTTCACTACCTGAGCAAAACAACAAAGTATGCTA 2394
 QY AsnValIThrValIAsnGIYGIYLYrAsnValIThrGIYLYrLeuAspLeuAsnTPTrTYrLeu 765
 Db 2395 AATGTCACTGTAAATGAGAGAGAAATGTAAACGAGAGCTAATCTTAACCTGGTACTTA 2454
 QY GIYIleTYrSerGIYLeuThrValAlaThrValLeuPheGIYIleAlaArgSerLeuLeu 785
 Db 2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATAGCAAGATCTCATATG 2514
 QY ValPheTYrValIleValIAsnSerSerGIYnYrLeuHleAsnLYsMePheGIYnYrIle 805
 Db 2515 GTATTCAGTCTCTGTATACTTCAACAACCTTGCAACAACAATGTTAGTCAAT 2574
 QY LeuLYsaIaIProValIleuPheAspArgAsnProIleGIYArgIleuAsnArgPhe 825
 Db 2575 CTGAAGAGCTCCGGTATTAATCTTTGATAGAAATCCAAATAGGAAGATTTTAATCGTTTC 2634
 QY SerLYsaAspIleGIYHleIeLeuAspAspLeuProLeuThrPheLeuAspPheIleGIYn 845

Db 2635 TCCAAAAGCATTTGACACTTGATGATGTTGCTGCCCTGACGTTTGTGATTTATTCAG 2694
 QY ThrLeuLeuGIYnValIleGIYValIseArValIAlaValIleProTrIleAla 865
 Db 2695 ACAATTCACAAAGT 2754
 QY IleProLeuValIProLeuGIYIleIlePheIlePheLeuArgArgTYrPheLeuGIYThr 885
 Db 2755 ATACCTTGTTCCCTTGGAGATCATTTTCAATTTTCTTCGGCGATATTTTGTGAAACG 2814
 QY SerArgAspValIYsaArgLeuGIYSerThrThrArgSerProValIseSerHleIseSer 905
 Db 2815 TCAGAGATGTGAAGCGCTGGAATCTCAACTCGAGATCCAGTGTTTTCCACATTCGCA 2874
 QY SerSerLeuGIYnGIYLeuTPTrThrIleArgAlaTYrLYrLYsaIleGIYnYrArgCYsGIYn 925
 Db 2875 TCTTCTCTCCAGGGGCTGTGACCATTCGGGCACTACAAAGCAAGAGGTGTCAAGAA 2934
 QY LeuPheAspAlaHleGIYAspLeuHleIseGIYAlaTPPheLeuPheLeuThrThSer 945
 Db 2935 CTGTTGTGACACACAGAGATTTACATTCAGAGGCTGTGTCTGTGTTTGAACAACGTCC 2994
 QY ArgTPPheAlaValArgLeuAspAlaIleCySaIaMetPheValIleIeValAlaPhe 965
 Db 2995 CGTGTGTGCGCGCTGCTGAGATGCACTGTGTGCAATGTTGTATCATCTGTGCTCTT 3054
 QY GIYSerLeuIleLeuAlaIYsaThrLeuAspAlaGIYnValIleGIYLeuAlaLeuSerTYr 985
 Db 3055 GGGTCCCGATTTCTGGCAAAAACCTGGATCCGGGCAAGTTGGTGGCATCTGCTAT 3114
 QY AlaLeuThrLeuMetGIYMeCPheGIYnTPCYsValIArgGIYnSerAlaGIYnValIleGIYn 1005
 Db 3115 GCCCTCAGCTCATAGGGGATGTTTCAGTGTGTGTTTCACAAGAGCTGAAGTTGAGAT 3174
 QY MetMetIleSerValGIYnArgValIleGIYrLYrThrAspLeuGIYnYsGIYnAlaProTr 1025
 Db 3175 ATGATGATCTCAGTGAAGAGGCTCATTAATAACACAGACCTTGAAGAAAGAACCTTGG 3234
 QY GIYrLYrGIYnYrArgProProProAlaTPProHleGIYnValIleIlePheAspAsn 1045
 Db 3235 GAATATCAGAAACGCCACCAACAGCTCGGCCCATGAAGAGGTATATCTTGACAT 3294
 QY ValAsnPheMetTYrSerProGIYGIYProLeuValIleuLYsHleLeuThrAlaLeuIle 1065
 Db 3295 GTGAACCTCATGTACAGTCCAGGTGGGCTCTGGTACGAAGCATCTCAACGACATCTCAT 3354
 QY LysSerGIYnGIYrLYrValIleValIleGIYrArgThrGIYrLYrLYsSerSerLeuIle 1085
 Db 3355 AAATCAAGAAAGAGGTGGCATGTGTGGGAAGAACGGAGCTGGAAAGATTCCTCATC 3414
 QY SerAlaLeuPheArgLeuSerGIYnProGIYnGIYrLYrIleTPTrIleAspLYsIleLeuThr 1105
 Db 3415 TCAGCCCTTTTAAATGTGTCAAGAACCGAAGGTAAATTTGGATGTATGATCTTGACA 3474
 QY ThrGIYnIleGIYLeuHleAspLeuArgLYsLYsMetSerIleIleProGIYnIleProVal 1125
 Db 3475 ACTGAATTTGACCTTCAGATTTAAGGAAGAAAGTCAATCACTCCAGAGAACCTGT 3534
 QY LeuPheThrGIYrLYrMetArgLYsAsnLeuAspProPheAsnGIYnIleThrAspGIYn 1145
 Db 3535 TTGTTCACCTGGAACATAGGAAAAAAGCTGGATTCCTTTAATGACACACGGATAGGAA 3594
 QY LeuTPPheAlaLeuGIYnValIleGIYnYrGIYnIleGIYnYrAspLeuProGIYLYS 1165
 Db 3595 CTGTGAATGTCTTACAGAGGTACAACTTAAAGAAACAATTGAAGATCTTCTGTGTA 3654
 QY MetAspThrGIYnLeuAlaGIYserGIYserAsnPheSerValIleGIYnArgGIYnLeuVal 1185
 Db 3655 ATGATATCTGAATGTAGCAAGATCAGATCCAAATTTTATGTGTGGCAAGAACATGTGGT 3714
 QY CySLeuAlaArgAlaIleLeuArgLYsAsnGIYnIleLeuIleIleAspGIYnAlaThrAla 1205
 Db 3715 TGCCTTGGCAAGGCAATCTCAGGAAAAATCAGATTTGATTTATGATGAAGCGACGGCA 3774


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Db      1162 ATCATCGTGTGTGACCTTCAACCACTACGTCCTCGGAGGTGATCAAGCAAC
QY      350 ArgValAlpheValAlValThrLeuYrGlyAlaValArgLeuThrValThrLeuPhePhe
Db      1222 CGCGGTTCGTGGCGAGTGAAGCTGTATGGAGCTGTGGCGGTGAAGCTTCTTCTTC
QY      370 ProSerAlaIleGluValArgValSerGluAlaIleValSerIleArgArgIleGlnThrPhe
Db      1282 CCTCAGCAGCATTTGAGGGGTGTCAAGGGCAATGTCAGCATCCGAAGATCCAGACCTTT
QY      390 LeuLeuLeuAspGluIleSerGlnArgAlaArgGlnLeuProSerAspGlyIleValMet
Db      1342 TTGCTACTTGATGAGATATCAAGCGCAACCGTCAGCTCCGTCAGATGTATAAAGAAG
QY      410 ValHisValIleAspPheThrAlaPheTyrAspIleValSerGlnThrProThrLeuGln
Db      1402 GTGCAATGTGAGAGATTTTACTGCTTTTGGATAMGGCATCGAGACCCCAACTTCAAA
QY      430 GlyLeuSerPheThrValArgProGlyGluLeuValAlaValGlyProValGlyAla
Db      1462 GGCCTTTCCTTACTGTCAAGACTGGCGAATTTGTAGCTGTGGTGGCCCGTGGGAGCA
QY      450 GlyIleSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuVal
Db      1522 GGGAGTCACTCACTGTTAAGTCCGTGCGGGGAATTTGGCCCAAGTCAAGCGCTGCTC
QY      470 SerValHisGlyArgIleAlaTyrValSerGlnGlnProTyrValPheSerGlyThrLeu
Db      1582 ACGCGTCATGAGAAATTCCTATGTCTTCAGCAAGCCCTGGGTGTTCTGGGAACCTCTG
QY      490 ArgSerAsnIleLeuPheGlyIleValYrGlyIleValYrGlyIleValYrGlyIleValYr
Db      1642 AGGAGTAATATTTATTTATTTGGAGAAATACGAAAGAAAGCAATATGAAAGTCAATAAAG
QY      510 AlaCyAlaLeuLeuValYrAspLeuGlnLeuLeuGlnAspGlyAspLeuThrValIleGly
Db      1702 GCTTGGCTCTGAAAGAAAGATTTTACGCTGTGGAGATGTGATCTGTGATAGGA
QY      530 AsparGlyIleThrThrLeuSerGlyGlyGlnYrAlaArgValAsnLeuAlaArgAlaVal
Db      1762 GATCGGGAAACCAACCTGATGAGGAGGCAAGAAAGCAAGGATTAACCTTCAAGAGCAAGT
QY      550 TyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluVal
Db      1822 TATCAAGATGTGACATCTATCTCTGAGCAATCTCTCAAGTCAATAGTGGGAAGT
QY      570 SerArgHisLeuPheGlyLeuLeuValIleGlyGlnIleLeuHisGlyIleThrIleLeu
Db      1882 ACGACAGACATTTGTCAACCTGTATTTGTCAAAATTTTCATGAGAAATCAAAATTTTA
QY      590 ValThrHisGlnLeuGlnTyrLeuValAlaIleSerGlnIleLeuIleLeuValAspGly
Db      1942 GTGACCTCATCACTGTGAGTCACTCAAGCTGCAAGTCAAGTTCATATTTGAAGATGT
QY      610 LysMetValGlnIleGlyIleTyrThrGlnPheLeuValSerGlyIleAspPheGlySer
Db      2002 AAAATGTGTCAAGAAAGGGAAGTCACTGAGTTCTTAAATCTGTATTAATTTTGGCTCC
QY      630 LeuLeuValYrAspAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln
Db      2062 CTTTTAAAGAGATATATGAGAAAGTGAACAACCTTCAGTTCAGAACTCCCACTCACTA
QY      650 ArgAsnArgThrPheSerGlu 656
Db      2122 AGGAATCGTACTTCTCAAG 2142

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; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-124-367A-148

Alignment Scores:
Pred. No.: 5,42e-304 Length: 2256
Score: 3262.00 Matches: 655
Percent Similarity: 87.9% Conservative: 0
Best Local Similarity: 87.9% Mismatches: 1
Query Match: 48.1% Indels: 90
DB: 12 Gaps: 1

US-09-976-858-42 (1-1325) x US-11-124-367A-148 (1-2256)
QY      1 MetLeuProValTyrGlnGluValIleProAsnProLeuGlnAspAlaAsnLeuCySer 20
Db      22 ATGCTGCCCGTGTACAGAGAGGTGAAGCCCAACCGCTGACAGAGCGAAGCCTGTCTCA 81
QY      21 ArgValAlphePheTrp----- 25
Db      82 CGCGGTCTCTCTG-ATGAGATCTGCTGTGTACCCAGCTGAGTGAAGTGGCGCACT 140
QY      25 ----- 25
Db      141 CTGACGTCACTGACAGCTTCACCTCTGTGTTCAGAGAGTCTCTGCTGACGACCAG 200
QY      25 ----- 25
Db      201 ACTAGAGGTCTCCCGCTCTTCTTCTTGAAGACACTTGCATTTGATTTAGACCA 260
QY      25 ----- 25
Db      261 CTGGATTAATCCAGATGATGTCTTCACTCCAACTCTCACTTTAATTCATGTGCAA 320
QY      26 -----TriLeuAsnProLeuPhe 31
Db      321 TACCTTTTCCAAATTAATTCATTTCTTTACAGAAAGGTGCTCAATCCCTGTTT 380
QY      32 LysIleGlyHisIleValArgArgLeuGlnGlnAspAspMetTyrSerValLeuProGluSer 51
Db      381 AAAATTTGGCATAAACGAGATTTAGAGAAAGTGTATGTATCTGCTGTCACAAAGAC 440
QY      52 ArgSerGlnHisLeuGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 71
Db      441 CGCTCAAGCACCTTGGAGAGAGTTCAGAGGTTCTGGATTAAGAAAGCTTTTAAAGAGCT 500
QY      72 GluAsnAspAlaGlnIleAspProSerLeuThrArgAlaIleIleLysCySerTyrTrpLysSer 91
Db      501 GAGATTAAGCACAGAAAGCTTTCTTAAACAAGCAATCATTAAGTGTACTGAAATCT 560
QY      92 TyrLeuValLeuGlyIlePheThrLeuIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 111
Db      561 TATTTAGTTTGGAGATTTTTCGTTAATTTGAGAAAGTCCAAAGTATTCAGGCCCTA 620
QY      112 PheLeuGlyIleIleIleAsnTyrPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 131
Db      621 TTTTGGGAAATTAATTAATTTTGTGAAATTAATGATCCATGATTTCTGTGGCTTGG 680

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132 AenThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIleLeuAlaIleLeu 151
 Db AACACAGCGGTACCGCTATGCGACGGTGTGACCTTTTGACCGCTCATTTGGCTTACAG 740
 152 HisHisLeuTyrPheTyrHisValGlnCysValAGlyMetArgLeuArgValAlaMetCys 171
 Db CATCATCTTATATTTTATCATCGTTACGTTGCTGGGATAGAGTTACGATTCAGCATGTGC 800
 172 HisMetIleTyrArgValAlaLeuArgLeuSerAspMetAlaMetGlyTyrThrThrThr 191
 Db CATATGATTTATTCGGAAGGACCTGCTCTTACTTAACTGCGCATGGGGAAGCAACACAA 860
 192 GlyGlnIleValAspLeuLeuSerAspValAspValAspPheAspGlnAlaThrValPhe 211
 Db GGCCAGATATGCAATCTGCTGTCATATGATGATGAACTTTGATCAGGTGACAGGTTC 920
 212 LeuHisPheLeuThrAlaGlyProLeuGlnAlaIleAlaValThrAlaLeuLeuThrPhe 231
 Db TTACACTTCTGCTGGGACGACGACCTGCGAGATTGCGATGACGCTGCTTACTGAGATG 980
 232 GlnIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIleIleLeuLeuProLeuGln 251
 Db GAGATAGGAATATCGTGCCTGCTGCGGATGCGAGTTCTATCATCTCTCGCCCTTGCAA 1040
 252 SerCysPheGlyIleLeuLeuPheSerLeuArgSerIleThrAlaThrPheThrAspAla 271
 Db AACTGTTTGGGAAGTTGTTCTCATCATCAGAGAGTAAACGCACTTTCACGAGATGCG 1100
 272 ArgIleArgThrMetAspGlnValIleThrGlyIleArgIleIleIleMetTyrAlaThr 291
 Db AGGATCAGACCATGATATGATATTAAGTTATTAAGATATTAATAATGATACCGCTGG 1160
 292 GlnIleSerPheSerAspLeuIleThrAspLeuArgValGlyGlnIleSerIleIleLeu 311
 Db GAAAGTCACTTTTCAATCTTATTAACAATTTGAGAAAGAGAGATTTCCAAGATTTGCG 1220
 312 ArgSerSerCysLeuArgIleMetAspLeuAlaSerPhePheSerAlaSerIleIleIle 331
 Db AAGAGTCTGCTGCTCAGAGGATGAAATTTGGCTTCAATTTTTCAGTCAAGCAAAATCAG 1280
 332 ValPheValThrPheThrThrTyrValLeuLeuGlySerValIleThrAlaSerArgVal 351
 Db GTGTTTGTACCTTCAACCACTTACGTCCTCTCGGACGTGATATCACGCCGCGCGTG 1340
 352 PheValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSer 371
 Db TTCGTGGCAGTGACGCTGATAGGGGCTGCGGCTGACGTTACCTCTTCCCTCA 1400
 372 AlaIleGlnArgValSerGlnAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 391
 Db GCCATTGAGAGGGGTGCAGAGGCAATCTGCACATCCGAAGATCCAGACCTTTTGGCTA 1460
 392 LeuAspGlnIleSerGlnArgAspArgIleLeuProSerAspGlyValAlaMetValHis 411
 Db CTTGATGAGATATCACAGCGCAACCTGCGCTGCGCTCGATGATGATTAAGATGTGTGAT 1520
 412 ValGlnAspPheThrAlaPheThrAspValAspArgIleThrProThrLeuGlnIleLeu 431
 Db GTGCAAGATTTTACGCTTTTGGGATAGGATCAGAACCCCAACCTTCAAGGCGCTT 1580
 432 SerPheThrValArgProGlyIleLeuLeuAlaValAlaGlyProValGlyValAGlyVal 451
 Db TCCCTTATCTGTCAGACCTGCGCAATTTGTAGCTGTGTGCGGCCCTGCGAACAAGGAG 1640
 452 SerSerLeuLeuSerAlaValLeuGlyIleLeuAlaProSerHisGlyLeuValSerVal 471
 Db TATATCTTATTAAGTCCGTGCTCGGAGATTTGGCCCAAGTACCGGCTGTGCTACCGTG 1700
 472 HisGlyArgIleAlaIleValSerGlnGlnProThrValPheSerGlyThrLeuArgSer 491
 Db CATGGAAGATTTGCTATGTGTCTCAGACGCGCTGCTGTCTCGGGAACCTGAGAGAT 1760

492 AenIleLeuPheGlyIleValGlyTyrGlnIleValArgIleValIleValAlaCys 511
 Db AATATTTTATTTGGGAAGAAATATACAAAAGCAATATGAAAAAGCTATAAGGCTGT 1820
 512 AlaLeuIleValAspLeuGlnLeuLeuGlnAspGlyAspLeuThrValIleGlyAspArg 531
 Db GCTCGAAAAAAGATTTACACTGCTGTGGAGATGTGATCTGATGATGATGAGATCGG 1880
 532 GlyThrThrLeuSerGlyIleGlnIleValArgValAspLeuAlaArgAlaValIleArg 551
 Db GGAAACAGCTGAGTGGAGGCGAAGAACACGGGTAACTTTGCAAGAGAGCTGTATCA 1940
 552 AspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGlyValSerArg 571
 Db GATGCTGACATCTATCTCTGACATCTCTCTCACTGACATGATGCGGAATTGACGA 2000
 572 HisLeuPheGlnLeuCysIleCysGlnIleLeuHisGlyValIleThrIleLeuValThr 591
 Db CACTGTTTCAACTGTGATTTGTCAATTTTGCATGAGAAATATCAATTTTACTGACT 2060
 592 HisGlnLeuGlnTyrLeuLeuValAlaAspSerGlnIleLeuIleLeuValAspGlySerMet 611
 Db CATCAGTTCAGTACCTTCAAAAGCTGCAAGTCAAGATTCGATATGAAAGATGTAAATG 2120
 612 ValGlnIleGlyIleThrTyrThrGlnPheLeuIleSerGlyIleAspPheGlySerLeuLeu 631
 Db GTGCAAGAGGAGCTTCACTGAGTCTTAAATTTGATATGATTTTGGCTCCCTTTTA 2180
 632 LysIleAspAspGlnIleSerGlnIleProValProGlyThrProThrLeuArgAsn 651
 Db AAGAAAGATATGAGAAAGGAAAGCAACCTCAGTTCCAGGAATCCCACTAAGAAAT 2240
 652 ArgThrPheSerGln 656
 Db GTTACCTTCTCAGAG 2255

RESULT 8

US-10-826-585-35

; Sequence 35, Application US/10826585
 ; Publication No. US20060008807A1

GENERAL INFORMATION:

; APPLICANT: Immunivest Corporation
 ; APPLICANT: O'Hara, Shawn Mark

; APPLICANT: Foulik, Brad

; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and

; FILE REFERENCE: IMNC 143 PCT/US

; CURRENT APPLICATION NUMBER: US/10/826,585

; PRIOR FILING DATE: 2004-04-16

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; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: 60/330669

; PRIOR FILING DATE: 2002-11-26

; PRIOR APPLICATION NUMBER: PCT/US02/26867

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn version 3.3

; LENGTH: 5011

; TYPE: DNA

; ORGANISM: Human

US-10-826-585-35

Alignment Scores:

Pred. No.:	2,816-209	Length:	5011
Score:	2285.50	Matches:	528
Percent Similarity:	56.6%	Conservative:	274
Best Local Similarity:	37.3%	Mismatches:	491
Query Match:	33.7%	Indels:	124
DB:	7	Gaps:	30

US-09-976-858-42 (1-1325) x US-10-826-585-35 (1-5011)

QY	3	ProValTyrGlnGlnVal-----LysPheAsnProLeuGlnAsp-----AlaAsnLeu	18
Db	782	CCCCGTCCTCGGAAACCATCCAGACCCCTTAATCCCTGCCAGCAGTCGACGCTTCCTTC	841
QY	19	CysSerArgValAlaPhePheTyrTrpLeuAsnProLeuPheLysIleGlnIleLysArgArg	38
Db	842	CTGTCGAGGATCACCTTCCTGGTGGATTCACAGGGTTGATTCGCGGGGCTTACCGCCAGGCC	901
QY	39	LeuGlnGlnAspAspMetTyrSerValLeuProGlnAspArgSerGlnIleLeuGlnGlu	58
Db	902	CTGAGGGGACAGTCAGCTCTGGTCTCTTAACAGAGAGACAGCTGGAAACAAGCTGTGCTT	961
QY	59	GluLeuGlnGlnLysPheTyrAspLysGln-----	67
Db	962	GTTTTTGGTAAAGAACTGGAGAGAGAAAGCCGCCAAGACTAGAGAGACGGGTGAAGTT	1021
QY	68	ValLeuArgAlaGlnAsnAspAlaGln-----	76
Db	1022	GTGTACTCTCCAGAGATCTGCCCCAGCGAAGAGAGACTTCAGAGTGATGCAATGAG	1081
QY	77	-----LysProSerLeuThrArg	82
Db	1082	GAGGTGGAGGCTTTGATGTCGTAAGTCCCCACAGAGAGGTGAACCCCTCTCTGTTAAAG	1141
QY	83	AlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlnIlePheThrLeuIleGlu	102
Db	1142	GTGTTATACAAAGACTTTGGGGCCCTACTCTCATGAGACTTCTTTCAAGGCCATCAC	1201
QY	103	GluSerAlaLysValIleGlnProIlePheLeuGlnLysIleIleAsnTyrPheGlnAsn	122
Db	1202	GACCTGATGATGTTTCCGGGCGCGAGATCTTA--AAGTTCCTATCAAGTGTGTGAT	1258
QY	123	TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr	142
Db	1259	-----GAGACGAGGCCCCCAACACATGGCAGGGCTACTTCAACCGTGTGCTG	1306
QY	143	PheCysThrLeuIleLeu--AlaIleLeuHisIleLeuTyrPheTyrHisValGlnCys	161
Db	1307	TTTTCACCTGCGCTGCTCCAGACCTCGTGGTCGACCGAGTCACTTCCATCTGCTTCGTC	1366
QY	162	AlaGlyMetArgLeuArgValAlaIleMetCysHisMetIleTyrArgLysAlaLeuArgLeu	181
Db	1367	AGTGCATGAGGATCATAAACGCGCTCATATTGGGCGTGTCTTACGAGGCCCTGTGATC	1426
QY	182	SerAsnMetAlaMetGlyLysThrThrThrGlnIleValAsnLeuSerAsnAsp	201
Db	1427	ACCAATTCAGCCAGAAATCTCCACCGGTGGGAGATTGTCAACTCATGTCTGTGGAC	1486
QY	202	ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProLeuGln	221
Db	1487	GCTCAGAGTTTCAGACTTGGCCACGATACATTAACTAGATCTGTGACGCCCTCTGCA	1546
QY	222	AlaIleAlaValThrAlaLeuLeuTyrMetGlnIleGlyIleSerCysLeuAlaGlyMet	241
Db	1547	GTGATCTCTTGGCTCTTACCTCTGTTGGCGTGAATCTGGGCCCTTCGCTCGGTGGAGATG	1606
QY	242	AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerLeu	261
Db	1607	GCGGTGAATGGTCTCTAGTGGTCCCGCTCAATGCTGTG-----ATG	1645
QY	262	ArgSerLysThrAlaThrPhe-----ThrAspAlaArgTlleArg	274
Db	1646	GCGATGAAGACCAACACGATAGGTAGGTGGCCCACTGAAGAGCAAGACAAATCGATCAAG	1705
QY	275	ThrMetAsnGlnValIleThrGlyIleArgIleIleLysMetTyrAlaTyrGlnLysSer	294
Db	1706	CTGATGAACGAAATTCATCATGGATTCAAAGCTTAAAGCTTAAAGCTGAGGACCTGGCA	1765
QY	295	PheSerAsnLeuIleThrAsnLeuArgLysLysGlnIleSerLysIleLeuArgSer	314
Db	1766	TTCAAGACAGAGTCTGGCCATCAGGACGAGAGCTGAAGTCTTAAGAAAGTCTTCC	1825

315 CysLeuNArgGlyMetAlaLeuAlaIAserPheheserAlaSerLysLleIleValIPheVal 334
|||
1826 TAACCTGCACGCCGGGGGACCTTCACCTGGGTCTGCACGCCCTTCTGTGGCTTGTGC 1885

335 ThrPheThrThrTyValIleLeu-----GlySerValIleThrAlaSerArgValPhe 352
|||||
1886 ACATTGGCCGCTACGTGACCATTCAGAGAAACAACATCTCGATGTCGACAGACCTTC 1945

353 ValAlaValThrLeuTyArgIlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
|||
1946 GTGCTTGTGGCCCTGTTCACATCTCCGGTTTCCCTGAACAT---CTCCCATGGTC 2002

373 IllegluArgValSerGluAlaIleValSerLleArgArgIlegIntThrPheLeuLeu 392
|||
2003 ATCCAGCAGCATCTGTCAGGACGAGGTCTCTCCCTCAAGCCCTGAGATCTTCTCCCAT 2062

393 AspGluIleSer-----GlnArgAsnArgIleuProSerAspGlyLysLys 408
:::|
2063 GAGAGAGCTGGAACTGCACAGCATGAGAGACGGCTCTCAAAAGACGGGGGGGACAGAC 2122

409 MetValHisValGlnAspPheThrAlaPheThrAspLysAlaSerGluThrProThrLeu 428
::|
2123 AGCATCACCGTAGAGGAATGACCACTTGCACCTGGGCGCAGG--AGCGACCTCCCACTG 2179

429 GlnGlyLeuSerPheThrValArgProGlyGluLeuAlaValValGlyProValGly 448
|||
2180 AATGGACATCACTTCTCCATCCCGAAGGTGCTTGTGGCGCGGTGGGGCAGGTGGC 2239

449 AlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeu 468
|||
2240 TGGCGAAGTGTCTCTCTCTCTCAGCCCTCTGSGCTGAGATGACAAAGTGGAGGGCAC 2299

469 ValSerValHisGlyArgIleAlaTyValSerGlnGlnProThrValPheSerGlyThr 488
|||
2300 GTGGCTATCAAGGGGCTCGGTGGCTATGTGCCACAGCAGGCGCTGATTCAGAAATGATCT 2359

489 LeuArgSerAsnIleLeuPheGlyLysAspTyTrpGluLysGluArgGlyTrpValIle 508
|||
2360 CTCCGAGAAACATCTCTTTGTGATGTACGTGAGAGAACCAATTAACAGTCCGTGATA 2419

509 LysAlaCysAlaLeuLysAlaAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIle 528
|||
2420 CAGGCTTGTCCCTCTCTCCAGACTGGAATCTCTGCCACGTGGGAGTCCGACAGAGATT 2479

529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAla 548
|||
2480 GGCGGAGAGGGCGTGAACCTGTCTGGGGGGCAGAGAGCGCGTGAAGCTGTGGCCGGGCG 2539

549 ValTyTrpGlnAspAlaAspLleTyLeuLeuAspAspProLeuSerAlaValAspAlaGlu 568
|||
2540 GTGATCTCCAAACCGTGACATTACTCTTCATATCTCCCTCTCAGCAGTGGAGTGGCCAT 2599

569 ValSerArgHisLeuPheGluLeuCysLleCysGln-----IleLeuHisGluLysIle 586
|||
2600 GTGGGAAAACAACATCTTTGAAAATGTGATTGGCCCCAAGGGAGTCTGAGAAACAAGACG 2659

587 ThrIleLeuValThrHisGlnLeuGlnTyTrpLeuLysAlaAlaSerGlnIleLeuLeu 606
|||
2660 CGGATCTTGTGCACGACACAGCATGAGCTACTTGGCGCAGGTGAGACGTCACTCATGTCATG 2719

607 LysAspGlyLysMetValGlnLysGlyThrTyThrTrpIleLeuLysSerGlyIleAsp 626
|||
2720 AGTGGCGGCAAGATCTCTGAGATGGGCTCTTACACGAGCGTGTGGCTCGAGACGGCGCC 2779

627 PheGlySerLeuLeuLys-----LysAspAsnGluGluSer 638
|||
2780 TTCGCTGAGTTCCTGCTGATCTATGCCACGACAGACGAGGACAGGATTCAGAGAGAGAAC 2839

639 GluGlnProProValProGly-----ThrProThrArgAsn----- 651
|||
2840 GGGGTGCACGGGCGTACGGCGTCCAGGAGAGAACAAAGCAATGAGAAATGCGATGCTG 2899

652 -----ArgThrPheSerGluSerSerValTrpSer 661

Db 2900 GTGACGACAGTGCAGGAGAACTGCAGACAGCTCAGGCTCCCTCCATAGT 2959
 Qy 662 GINGInserSerArgProserleuYsaBglYAlaLeuGInserGlnAspThrGluAn 681
 Db 2960 GGGGACATCAAGGACCAACAGACCGCAGAACTGCAGAAAGTCCAGGCCAAG 3019
 Qy 682 ValProVal---ThrleuSerGluGluAnArgSerGlu---GlyValGlyPheGln 699
 Db 3020 GAGGAGACCTGGAGAGTGAATGAGGCTGCAGAGGCCACAGAGGAGTCAAGCTTCC 3079
 Qy 700 AlaTyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPhe-----IlePheLeu 717
 Db 3080 GTGTACTGGACTACATGAAAGCCATCGGACTTCTCATCTCTCCAGCATCTTCCCT 3139
 Qy 718 IleleuLeuAsnThrAlaAlaGlnAlaAlaTyrValleuGlnAspTrpTrpLeuSerTyr 737
 Db 3140 TTCATGTGTAC-----CATGTGTCGGCTGGCTTCCACACTATTTGGCTCAGCCCTC 3190
 Qy 728 TrpAlaAsnLysGInserMetLeuAsnValThrValAsnGlyGlyValAsnValThrGlu 757
 Db 3191 TGGACTGAT-----GACCCCATCGTCAAGGAGCTCAGAGACACAGCA 3235
 Qy 758 ---LysleuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrVal 776
 Db 3236 GTCCGGCTGAGGCTCATATGAGGCTCGGCTGCAATTTCAAGGAGTGCCTG----- 3286
 Qy 777 LeuPheGlyIleAlaArgSerleuLeuValPheTyrValleuValAsnSerGlnThr 796
 Db 3287 ---TTTGGTACTCATGAGCCGTGTCATCGGAGGAGATCTTG-----GCTTCCGCTGT 3337
 Qy 797 LeuHisAsnLysMetPheGluSerIleLeuLysAlaProValleuPheAspArgAsn 816
 Db 3338 CTGCACGTGAGCTGTCAGACAGCATCTGCGGTCAACCCATGAGCTTCTTGAAGGAGCC 3397
 Qy 817 ProIleGlyArgIleleuAsnArgPheSerLysAspIleGlyHisleuAspAspLeu 836
 Db 3398 CCCAGTGGAGACCTGGTGAACGGCTTCTCCAGAGAGCTGACACAGTGAATCCATGATC 3457
 Qy 837 ProleuThrPheleuAspPheIleGlnThrleuLeuGlnValValGlyValValSerVal 856
 Db 3458 CCGGAGGTCATCAAGATGTTCAAGGCTCCCTGTTCAACGTCATGTCCTCCATCGT 3517
 Qy 857 AlaValAlaValIleProTrpIleAlaIleProleuValProleuGlyIleIlePheIle 876
 Db 3518 ATCTGCTGGCAACGCCCATCCGCCATCATCATCCGCCCTTGCTCATCTCACTTC 3577
 Qy 877 PheleuArgArgTyrPheleuGluThrSerArgAspValLysArgleuGlnSerThrThr 896
 Db 3578 TTCGTCCAGAGGTTCTACGTGCTTCTCCCGACGCTAGAGGCTCCAGATCGGTCAAC 3637
 Qy 897 ArgSerProValPheSerHisleuSerSerleuGlnGlyLeuTrpThrIleArgAla 916
 Db 3638 CGCTCCCGCGGTCAATCCCATTTCAACAGACCTTCTGCGGGGTCAAGCTCATTTGAGCC 3697
 Qy 917 TyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlu 936
 Db 3698 TTCGAGGACAGAGAGGCTTTCATCCACAGAGTACCTGAGGTGACAGAACAGCAAG 3757
 Qy 937 AlaTrpPheLeuPheleuThrThrSerArgTrpPheAlaValArgleuAspAlaIleCys 956
 Db 3758 GCTTATTACCCAGCATCGTGGCCACAGAGTGGCTGCGCTGCGGTGAGAGTGTGGGCG 3817
 Qy 957 AlamelPheValIleIleValAlaPheGlySerleuIleleuAlaLysThrleuAspAla 976
 Db 3818 AACTGCATGTTCTGTGCTGCTGCTGTTGGGTGATCTCCAGGACAGCGCTCAGTGT 3877
 Qy 977 GlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrleuMetGlyMetPheGlnTrpCys 996
 Db 3878 GCGTGGTGGCGCTTCAGATGTCCTTCACTATTCAGAGTCAACAGTACTGGAACCTGGCTG 3937
 Qy 997 ValArgGlnSerAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyr 1016

Db 3938 GTTCGATGTCATCTGAATGAGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGAGTAT 3997
 Qy 1017 ThrAspLeuGluLysGluAlaProTrpGluTyrGlnLys---ArgProProProAlaTrp 1035
 Db 3998 TCAGAGACTGAGAAAGAGGCGCCCTGTCGAATTCAGAGAGACAGCTCCGCCACAGAGCTGG 4057
 Qy 1036 ProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyPro 1055
 Db 4058 CCCAGAGTGGGCGGAGTGAATTCGGAACTACTGCTCGGCTACCGAGAGACCTTGAC 4117
 Qy 1056 LeuValleuLysHisleuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGly 1075
 Db 4118 TTCGTTCTCAGGACATCAATGATGTCAGTCAATGAGGAGAAAGTGGAGTGTGGGG 4177
 Qy 1076 ArgThrGlyAlaGlyLysSerSerleuIleSerAlaLeuPheArgLeuSerGlu---Pro 1094
 Db 4178 CGAGCGGAGCTGGAGATGCTCCCTGACCTCGGCTTATTTCCGATACAGAGTCTGCC 4237
 Qy 1095 GlnGlyLysIleTrpIleAspLysIleleuThrThrGluIleGlyLeuHisAspLeuArg 1114
 Db 4238 GAGGAGAGATCATCATGATGAGATCAACATCCGCAAGATCGGCTGCAGACTCCGC 4297
 Qy 1115 LysLysMetSerIleIleProGlnGluProValleuPheThrGlyThrMetArgLysAsn 1134
 Db 4298 TTCAGATCAACATCATATCCCGAGGACCTGTGTTGTTTGGGTTCCTCCGATGAAAC 4357
 Qy 1135 LeuAspProPheAsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGln 1154
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 Qy 1155 LeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAlaGlnSerGly 1174
 Db 4418 CTGAAGACTTCGTGTACAGCCCTTCTCTGAACAAGTACAGTAAATGTCAGAAAGCGGG 4477
 Qy 1175 SerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleleuArgLys 1194
 Db 4478 GAGAACTCAAGTGTGGGACAGCGCCACTTGTGTGCTTACGACCGGCGCTGAGGAAG 4537
 Qy 1195 AsnGlnIleleuIleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeu 1214
 Db 4538 AGGAAGATCTTGTGTGATGAGGCAACGCGACCGTGCACCTGGAACGAGACGACTC 4597
 Qy 1215 IleGlnLysLysIleArgGluLysPheAlaHisCysThrValleuThrIleAlaHisArg 1234
 Db 4598 ATCCAGTCCACATCCGAGACACAGTTCAGAGACTGACCGTCTCAACATGCCACCGG 4657
 Qy 1235 LeuAsnThrIleleuAspSerAspLysIleMetValleuAspSerGlyArgleuLysGlu 1254
 Db 4658 CTCACACATCATGATGATACACAAAGGTGATCGTTCGACAAAGGAAATCAGAGAG 4717
 Qy 1255 TyrAspGluProTyrValleuLeuGlnAsnLysGlnSerleuPheTyrLysMetValGln 1274
 Db 4718 TACGCGGCCCATCGAGACTCTCTGCACAGAGAA---GGCTTTTCTTACAGATGCGCAA 4774
 Qy 1275 GlnleuGly-----LysAlaGlnAlaAlaIleleuThrGluThrAlaLysGlnVal 1291
 Db 4775 GAGCCGCGCTGGTGTGAGCCCAAGAGCTGGCATATCTGTGTCAGAACTGAGGCGCTATA 4834
 Qy 1292 Tyr-----PheLysArgAsnTyrProHisIleGlyHisThrAspHisMetValThr 1308
 Db 4835 TGCCAGCGCCAGGAGAGATGATGATCCCTG-GRAAACAAAGCTCCACAGTGAAC 4893
 Qy 1309 AsnThrSerAsnGlyLysProSerThrleuThrIleIleGlnThrAla 1324
 Db 4894 AAAACATAAAAACCAAAACCAAGACAAACCAAAACATTTCAAGAGCA 4941
 RESULT 9
 US-11-045-578-3
 ; Sequence 3, Application US/11045578
 ; Publication No. US20060024685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HO, Rodney J.Y.
 ; APPLICANT: YANG, Ziping

```

APPLICANT: SHEN, Danny D.
APPLICANT: WU, Daniel
TITLE OF INVENTION: NOVEL SEQUENCE VARIANTS OF MULTI-DRUG RESISTANCE GENES, MDR1 AND
TITLE OF INVENTION: MRP1, AND RECOMBINANT CELLS EXPRESSING MRP1 AND MDR1 FOR
TITLE OF INVENTION: ASSESSMENT OF DRUG PENETRATION AND DISPOSITION
FILE REFERENCE: 016336-002510US
CURRENT APPLICATION NUMBER: US/11/045,578
PRIOR FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: US 60/539,362
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 5011
TYPE: DNA
ORGANISM: human
US-11-045-578-3

Alignment Scores:
Pred. No.: 2,81e-209 Length: 5011
Score: 2285.50 Matches: 528
Percent Similarity: 56.6% Conservative: 274
Best Local Similarity: 37.3% Mismatches: 491
Query Match: 33.7% Indels: 124
DB: Gaps: 30

US-09-976-858-42 (1-1325) x US-11-045-578-3 (1-5011)

QY 3 ProValTYrGlnGluVal-----LYsProAnProLeuGlnAsp-----AlaAsnLeu 18
DB 782 CCCCTGTTCTCGAAGCCATCCAGCAGCCCTAATCCCTGCGCAGAGCCGCTTCCTTC 841
QY 19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheValIleGlyHisArgArg 38
DB 842 CTGTCAAGATACCTCTGTGTGATCAAGAGTTATGTCGGGGATCCAGCCAGCC 901
QY 39 LeuGlnGluAspAspMetTrpSerValLeuProGluAspArgSerGlnHisLeuGln 58
DB 902 CTGAGGCGAGTGAACCTGTGCTTAAACAAGAGACACGTGGGAACAGTCGTGCT 961
QY 59 GluLeuGlnGlyPheTrpAspArgGlu----- 67
DB 962 GTTTTGTTGAAGAACTGGAAGAAAGATGCGCCAGACTAGAACGCCGGTGAAGTT 1021
QY 68 ValLeuArgAlaGluAsnAspAlaGln----- 76
DB 1022 GTGTACTCTCCAGGATCTGCGCCAGCGAAGAGATTCAGAGTGATGCGAATGAG 1081
QY 77 -----LYsProSerLeuThrArg 82
DB 1082 GAGGTGAGGCTTTGATCGTCAAGTCCGACAGAAAGAGTGAAGACCCCTCTGTTTAA 1141
QY 83 AlaIleIleGlyCysTrpTrpLysSerTrpLeuValLeuGlyTrpPheThrLeuIleGlu 102
DB 1142 GTGTATACAAAGACCTTGGGCGCTTACTTCATAGCTCTTCTTCAAGCGCATCCAC 1201
QY 103 GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTrpPheGluAsn 122
DB 1202 GACCTGATGATGTTTCCGGGCGGACAGATCTTA--AAGTGTCTACCAAGTTCTGAT 1258
QY 123 TyrAspProMetAspSerValAlaLeuAsnThrAlaTrpAlaThrValLeuThr 142
DB 1259 -----GACACGAAGGCCGACGCTGGCAGCGGCTTCAACCGTGGCTGCG 1306
QY 143 PheCysThrLeuIleLeu--AlaIleLeuHisLeuTrpPheTrpHisValGlnCys 161
DB 1307 TTGTGACAGCTGCTGCGAGACCCCTGCTGCTGCACAGTACTTCCACATCTGCTTCC 1366
QY 162 AlaGlyMetArgLeuArgValAlaMetCysHisMetIleTrpArgValAlaLeuArgLeu 181
DB 1367 AGTGCGATGAGTACCAAGACCGCTGCTGATGGGGCTGTATCGAAGGCCCTGTGGATC 1426
QY 182 SerAsnMetAlaMetGlyLysThrThrThrGlnIleValAsnLeuSerAsnAsp 201

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DB 1427 ACCAATTGACGAGAAATCTCCAGCGTGGGAGATGTCACTCATCTATCTGTGGAC 1486
QY 202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
DB 1487 GCTCAGAGCTTCAAGGACTTGGCCAGCAGTCAATTAATGATCTGTGACGCCCTCGAA 1546
QY 222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
DB 1547 GTCACTCTGCTCTCACTCTGCTGCTGAATGAGGCGCTTCCGCTGCTGCTGAGTGG 1606
QY 242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
DB 1607 GCGGTGATGCTCTCATGTGCTCCGCTCAATGCTGTG-----ATG 1645
QY 262 ArgSerLysThrAlaThrPhe-----ThrAspAlaArgIleArg 274
DB 1646 GCGATGAAGACCAAGACCTATCAAGTGGCCCAATGAAGCAAGCAATCGATCAAG 1705
QY 275 ThrMetAsnGluValIleThrGlyIleArgIleIleLeuMetTrpAlaTrpGluLysSer 294
DB 1706 CTGATGAACGAATCTCATATGGATCAAGTGTAAAGCTTTATGCTTGGAGAGCTGGCA 1765
QY 295 PheSerAsnLeuIleThrAsnLeuArgLysGluIleSerLysIleLeuArgSerSer 314
DB 1766 TTCAAGGACAAAGTGTGCTGCCATCAGGACGAGAGAGCTGAAGGTCTGAAGAGCTGCC 1825
QY 315 CysLeuArgGlyMetAsnLeuAlaSerPheSerAlaSerLysIleIleValPheVal 334
DB 1826 TACCTTGACCGCGTGGGACCTTCACTGAGTGTGCACGCCCTTCTGTGCTTGGC 1885
QY 335 ThrPheThrThrTrpValLeuLeu-----GlySerValIleThrAlaSerArgValPhe 352
DB 1886 ACATTGCGGTCTAGTACCATGACGAGAAACAACATCTGATGCGCCAGACAGCTTC 1945
QY 353 ValAlaValThrLeuTrpGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
DB 1946 GTGTCTTGGGCTGTTCAACATCTCCGCTGTTCCCTCGAAGCATTT--CTCCCATGCTC 2002
QY 373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 392
DB 2003 ATCAAGACAGCTGTGAGGACAGAGTGTCTCCCTCAAAACCTGAGAGATTTTCTCCCAT 2062
QY 393 AspGluIleSer-----GlnArgAsnArgGlnLeuProSerAspGlyLysLys 408
DB 2063 GAGAGGCTGGAACCTGACAGATGACGAGAGGCTGTCAAAAGCGGGGGGACGAGAC 2122
QY 409 MetValHisValGlnAspPheThrAlaPheTrpAspLysValAspGluThrProThrLeu 428
DB 2123 AGCATCACCGTAGAGAAATGACACATTCACCTGGGCGAAG--AGGACCTTCCACACTG 2179
QY 429 GlnGlyLeuSerPheThrValArgProGlyLeuLeuAlaValIleGlyProValGly 448
DB 2180 AATGGCATCACCTTCTTCATCCCGAAGAGTCTTGGTGGGCGGTGGTGGGCGAGTGGGC 2239
QY 449 AlaGlyLysSerSerLeuLeuSerAlaValIleGlyGluLeuAlaProSerHisGlyLeu 468
DB 2240 TGGCGAAAGTGTCTCTCTCTCACTCTTGGTGTGAGATGAGCAAAAGTGGAGGGGAC 2299
QY 469 ValSerValHisGlyArgIleAlaTrpValSerGlnGlnProTrpValPheSerGlyThr 488
DB 2300 GTGGCTATCAAGGGGCTCGGTGCTATGTGCACAGCAGGCTGGATTCAGAAATATCT 2359
QY 489 LeuArgSerAsnIleLeuPheGlyLysLysTrpGlyLysGluArgGlyGlyValIle 508
DB 2360 CTCCGAGAAACATCTCTTTTGGATGTCACTGGAGCAACATATTAAGGTCCGTGTA 2419
QY 509 LysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIle 528
DB 2420 CAGGCTTGTGCTCTCTCCAGACTGGAATCTGCGCAATGGGAGTGGACAGAGTT 2479
QY 529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysValArgValAsnLeuAlaArgAla 548

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Db 2480 GCGGAGAGGCGTGAACCTGTCTG3GGGCGAAGACGCGTGAAGCCGCGGACC 2539
 Qy 549 ValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGln 568
 Db 2540 GTGTCTCCACGCGTGAACCTTTCATTCCTTTCATGATGATCCCTCTCAGCATGATGCCAT 2599
 Qy 569 ValSerArgHisLeuPheGluLeuGlyCysIleCysGln-----IleLeuHisGluLeu 586
 Db 2600 GTGGGAAAAACATCTTTGAAAATGATGATGGCCCCCAAGGGATCTGTAAGAAACAAAGACG 2659
 Qy 587 ThrIleLeuValThrHisGlnLeuGlnTyrLeuLeuValAlaSerGlnIleLeuIleLeu 606
 Db 2680 CGGATCTTGTCACCGACAGCATGAGCTACTTCCGAGTGAAGTCACTCATCTGATG 2719
 Qy 607 LysAspGlyLysMetValGlnLysGlyTyrTyrGlnPheLeuLysSerGlyIleAsp 626
 Db 2720 AGTGGCGGAAATGTCGATGATGGCTCTACAGAGCTGCTGCTGACAGCGCGCC 2779
 Qy 627 PheGlySerLeuLeuLeu-----LysAspAsnGlnGlnSer 638
 Db 2780 TTCCGTGATCTCTGCTACTTATCCAGACAGACAGACAGACAGATCCAGAGAAC 2839
 Qy 639 GlnGlnProProValProGly-----ThrProThrLeuArgAsn----- 651
 Db 2840 GGGGTACAGCGCGTCAAGCGCTCCAGGAAAGAAAGAAAGAAATGGCATGCTG 2899
 Qy 652 -----ArgThrPheSerGlnSerSerValTyrSer 661
 Db 2900 GTGACGACAGTGAAGGAAAGCACTGACAGACAGCTCAGACGCTCCCTCCATGAT 2959
 Qy 662 GlnGlnSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 681
 Db 2960 GGGGACATCAGAGGACCAACACAGACCGGCAATCTCAGAAAGCTGAGGCCCAAG 3019
 Qy 682 ValProVal-----ThrLeuSerGlnGlnLysAsnArgSerGln-----GlyLysValGlyPheGln 699
 Db 3020 GAGGAGACCTGAGAGCTGATGAGGCTGACAAAGGCGACAGAGGAGCTCAAGCTTCC 3079
 Qy 700 AlaTyrLysAsnTyrPheArgAlaGlyAlaHisTyrPheValPhe-----IlePheLeu 717
 Db 3080 GTGTCTGGAGCTACATGAAAGGCAATCGGACTCTTCATCTCTCTCAGCATCTTCTT 3139
 Qy 718 IleLeuLeuAsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrPheLeuSerTyr 737
 Db 3140 TTCATGTGTAC-----CATGTGTCCGCGCTGCTTCCAACTATTTGCTCAGCTCC 3190
 Qy 738 TrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGlyGlyLysValThrGln 757
 Db 3191 TGGACTGAT-----GACCCCATCGTCAAGGAGCTCAGAGACACAGAA 3235
 Qy 758 ---LysLeuAspLeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrVal 776
 Db 3236 GTCCGCGTGAAGCTGATGAGCCCTGGGCAATTTCAAAAGGATGCGCGT----- 3286
 Qy 777 LeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSerGlnThr 796
 Db 3287 ---TTTGGTACTCGATGCGCTGTCACCGGGGGATCTTG-----GCTTCCCGCTGT 3337
 Qy 797 LeuHisAsnLysMetPheGlnSerIleLeuLysValAlaProValLeuPhePheAspArgAsn 816
 Db 3338 CTGCAACGTGAGCTCTGTCAGACATCTGCGGCTCAACCATAGACTTTTGAAGCGGAC 3397
 Qy 817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeu 836
 Db 3398 CCCAGGTGGAACTGTGTGAACCGCTTCTCAAGAGCTGACAGACAGTGAATCCATGATC 3457
 Qy 837 ProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerVal 856
 Db 3458 CCGAGAGTCATCAAGATGTTCATGGCTCCCTGTTCACAGCTATTCAGTGGTCCATCGCT 3517
 Qy 857 AlaValAlaValIleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIle 876
 Db 3518 ATCTGCTGGCCACGCGCATCGCGCATCATTCGCGCCCTTGAGCTCTACTTCTC 3577

Qy 877 PheLeuArgTyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThr 896
 Db 3578 TTCTCCAGAGCTTCTAGCTGGCTTCTCCCGGACAGTGAAGCCCTGATCCGCTGAC 3637
 Qy 897 ArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTyrThrIleArgAla 916
 Db 3638 CGCTCCCGGCTATTCCTCATTTCAAGACATTTGCTGGGGGTGAGCGTCAATTCAGACC 3697
 Qy 917 TyrLysAlaGlnGlnArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGln 936
 Db 3698 TTCCAGAGACAGAGCGCTTTCATCCACAGATGACCTGAAGTGAAGAGACAGACAGAG 3757
 Qy 937 AlaThrPheLeuPheLeuThrThrSerArgThrPheAlaValArgLeuAspAlaIleCys 956
 Db 3758 GCTTATTCACCCAGATCTGTCGCGCCCAACAGTGGCTGGCCGCTGAGATGTGTGGGC 3817
 Qy 957 AlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAla 976
 Db 3818 AACTGACATGCTTGTGTTGCTGCGCTGTTGCGGATCTCCAGGACAGGCTCATGCT 3877
 Qy 977 GlnGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCys 996
 Db 3878 GGGTGGTGGGCTCTCAGTGTCTTACTCATTTGACAGGTCAACAGTACTGAACCTGCTG 3937
 Qy 997 ValArgGlnSerAlaGlnValGlnLysMetMetIleSerValGlnArgValIleGlnTyr 1016
 Db 3938 GTTCGATGATCATCGAATGAAACCAACATCGTGGCGGTGAAGAGCTCAAGAGATAT 3997
 Qy 1017 ThrAspLeuGlnLysGlnAlaProTyrGlnTyrGlnLys---ArgProProProAlaTyr 1035
 Db 3998 TCAGAGACTGAAGAGAGGCGCCCTGGGAATCCAGAGAGACAGCTCCGACAGACGCTGG 4057
 Qy 1036 ProHisGlnGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyPro 1055
 Db 4058 CCCGAGTGGGCGCAAGTGAATTCGGAATCTGCTGCTCCGCTCCGAGAGACCTTGAC 4117
 Qy 1056 LeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGlnLysValGlyIleValGly 1075
 Db 4118 TTCTGTTCCAGGCATCATCATGATGTCAGATCAATGGGGAGAAAGTGGCATCTGTGGG 4177
 Qy 1076 ArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGln---Pro 1094
 Db 4178 CCGAGGAGAGCTGGGAATCTCTCCCTGACCTGGGCTTATTTCCGATGAAGAGCTGCC 4237
 Qy 1095 GlnGlyLysIleTyrPheAspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArg 1114
 Db 4238 GAAAGAGATCATCATGATGATGATCAATCCGCAAGATCGGCTGACAGACTCCGC 4297
 Qy 1115 LysLysMetSerIleIleProGlnGlnProValLeuPheThrGlyThrMetArgLysAsn 1134
 Db 4298 TTCAAGATCACATCATCTCCAGAGACCTGTGTGTGTGTGTGGTTCCTCCGATGATAC 4357
 Qy 1135 LeuAspProPheAsnGlnHisThrAspGlnGlnLeuTyrPheAlaLeuGlnGlnValGln 1154
 Db 4358 CTGACCCATTCAGCAGTACTCGATGAAGAAGCTGAAGCTCCCTGAAGCTGCCAC 4417
 Qy 4418 CTGAAGAGCTTGGTGTGACCTCTCTCTGCAAGCTGAAGCCTGAATGCGAAGGCGGG 4477
 Qy 1175 SerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLys 1194
 Db 4478 GAGAACTCAAGTGTGCGGACGCGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4537
 Qy 1195 AsnGlnIleLeuIleIleAspGlnAlaThrAlaAsnValAspProArgThrAspGlnLeu 1214
 Db 4538 ACGAAGATCTTGT 4597
 Qy 1215 IleGlnLysLysIleArgGlnPheAlaHisCysThrValLeuThrIleAlaHisArg 1234
 Db 4598 ATCCAGCTCACACATCCGACAGATGGAAGATGAGACCTGCTCAGCATGCGCCACCGG 4657

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DB 4658 CTCACACCATCATGACATACACACAGGGTATGCTTGGACAAAGAGAAATCCAGAG 4717
QY 1255 TyrAspGluProTyrValleuIleuGlnAenIysGluSerLeuPheTyrIysMetValGln 1274
DB 4718 TAGGCGGCCCATCGACCTCTGCGACGAGAGA---GGCTTTTCTACGACTGGCCAAA 4774
QY 1275 GlnIleuGly-----LysAlaGluAlaAlaIleuThrluThrlAlaIysGlnVal 1291
DB 4775 GACGCGGGTGTGTGTGAGCCCGACAGCTGCATATCTGTGCAGACTGCGAGGCTATA 4834
QY 1292 Tyr-----PheIysArgAsnTyrProHisIleGlyHisThrAspHisMetValThr 1308
DB 4835 TCCGACGCGCCAGGAGAGAGTCACTCCG-GTAAACCAAGCCTCCACACACTGAACC 4893
QY 1309 AsnThrSerAsnGlyGlnProSerThrIleuThrllePheGluThrAla 1324
DB 4894 AAAACGTAAAAACCAAAACCCAGACAAACCAATATTCAAGCAGCA 4941

RESULT 10
US-11-045-578-2
/ Sequence 2, Application US/11045578
/ Publication No. US20060024685A1
/ GENERAL INFORMATION:
/ APPLICANT: HO, Rodney J.Y.
/ APPLICANT: YANG, Ziping
/ APPLICANT: SHEN, Danny D.
/ APPLICANT: MU, Daniel
/ TITLE OF INVENTION: NOVEL SEQUENCE VARIANTS OF MULTI-DRUG RESISTANCE GENES, MDR1 AND
/ TITLE OF INVENTION: MRP1, AND RECOMBINANT CELLS EXPRESSING MRP1 AND MDR1 FOR
/ FILE REFERENCE: 016336-002510US
/ CURRENT APPLICATION NUMBER: US/11/045,578
/ PRIOR FILING DATE: 2005-01-26
/ PRIOR APPLICATION NUMBER: US 60/539,362
/ PRIOR FILING DATE: 2004-01-26
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 2
/ LENGTH: 4587
/ TYPE: DNA
/ ORGANISM: mouse
/ US-11-045-578-2

Alignment Scores:
Pred. No.: 3,76-207 Length: 4587
Score: 2263.00 Matches: 491
Percent Similarity: 57.3% Conservative: 288
Best Local Similarity: 36.1% Mismatches: 468
Query Match: 33.3% Indels: 112
DB: 12 Gaps: 23

US-09-976-858-42 (1-1325) x US-11-045-578-2 (1-4587)

QY 3 ProValTyrGlnGluVal-----LysProAsnProLeuGlnAspAlaAsnLeu 18
DB 586 CCCCTGTTCTGAAACTGTCATGACCGGAATCCATGCCAGAAATCCAGTCCCTTTC 645
QY 19 CysSerArgValPhePheThrTrpLeuAsnProLeuPheIleGlyHisLysArgArg 38
DB 646 CTTTCCAGGATTACTTCTGTGATTAACAGGATGATGTCAGCGCTACCGCAGCC 705
QY 39 LeuGluGluAspAspMetTyrSerValleuProGluAspArgSerGlnHisLeuGlu 58
DB 706 CTGGAAGAGAGTGAACCTCTGCTGATTAAGAGAGACACATCAGAAAGAGTGAACCT 765
QY 59 GlnLeuGlnGlyPheThrAspIysGlu----- 67
DB 766 GTGCTGTGAATTAATCTGAAGAAAGAAATGTGATTAAGTCAAGAGAGCGCTGACGATT 825
QY 67 ----- 67

DB 826 GTGATGCGCCCTCCCAAGATCCAGACAGCTAAAGGAATTCOCAGTTGATGTGAT 885
QY 68 -----ValleuArgAlaGluAsnAspAlaGlnIysProSerLeuThr 81
DB 886 GAGAGGTGAGAGCAGTATGTGATCAAGTCAACCCACAGAGATCGGAGCCCTCTGTTTC 945
QY 82 ArgAlaIleIleIysCysTyrTrpIysSerTyrIleuValleuGlyIlePheThrLeuIle 101
DB 946 AAGGTGTATACAAAGACTTTGTGCTTCACTTCCATGAGCTTCCTGTACAGGCCCTT 1005
QY 102 GluIleuSerAlaIysValIleGlnProIlePheLeuGlyIleIleAsnTyrPheGlu 121
DB 1006 CATGACCTGATGATCTTGGCCGCCCAAGATCTTGAATGATTAATCACTGTGTGAT 1065
QY 122 AsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValleu 141
DB 1066 GACAGGAGAGGCTCCGACCTGG-----CAGGCTACTTTTACAGACAGCTGCTG 1113
QY 142 ThrPheCysThrLeuIleLeuAlaIleuHisIleuTyrPheTyrHisValGlnCys 161
DB 1114 TTTGTACGCGCCTGTCTGACAGACACTGACCTCCACAGTACTTTCATATCTGCTGCTC 1173
QY 162 AlaGlyMetArgLeuArgValAlaIleCysHisMetIleTyrArgIysAlaIleuArgLeu 181
DB 1174 AGTGCATGCGCATACAAAGCTGTGTGTGAGCGCTGTCTATCTGAAGCTCTTTGATC 1233
QY 182 SerAsnMetAlaMetGlyIysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201
DB 1234 ACCAATGACGTAGAAATCTTCCACGCGTCCGAGAGATTTGCAACCTCATGTCCGTGAT 1293
QY 202 ValAsnIysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProLeuGln 221
DB 1294 GCTCAGCCCTTCAAGACTGTGCGCACGTAACATTAACATGATGTGTCAGCCCTCTGAA 1353
QY 222 AlaIleAlaValThrAlaLeuLeuThrPheMetGluIleGlyIleSerCysLeuAlaGlyMet 241
DB 1354 GTCACTCTAGCCCTTACTTCTGTGTGAGCTGAGCCCTTCTGTGCTGCTGAGTGC 1413
QY 242 AlaValleuIleIleLeuLeuProLeuGlnSerCysPheGlyIysLeuPheSerSerLeu 261
DB 1414 GCTGTGATGATTTCTCATGTGTAACCTTAATGCTGTG-----ATG 1452
QY 262 ArgSerIysThrAlaThrPhe-----ThrAspAlaArgIleArg 274
DB 1453 GCCATGAAGACCAAGACCTACAGGTGCGACACATGAAGACAAAGACCAACCGAATCAAG 1512
QY 275 ThrMetAsnGluValIleThrGlyIleArgIleIleIysMetTyrAlaTrpGluIysSer 294
DB 1513 CTGATGAACGAGATCTCAATGGAGATCAAGTCTCAAGCTGTACGCTGGAGCTGGCC 1572
QY 295 PheSerAsnLeuIleThrAsnLeuArgIysIysGluIleSerIysIleLeuArgSerSer 314
DB 1573 TTCCAGACAAAGATCATAGCATCAGCAGGAGAGAGCTCAAGGTCTGAAGAAATCTGCC 1632
QY 315 CysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerIysIleIleValPheVal 334
DB 1633 TACCTGGACGCTGTAGGACATTCACGTGGGTGTCACACTTCTGTGGCCCTGTCA 1692
QY 335 ThrPheThrThrTyrValleuLeuGly-----SerValIleThrAlaSerArgValPhe 352
DB 1693 ACCTTTGTCTGTGTGTGATGATGATGAGAAATATCTTAAGATCAAGAAAGACCTTT 1752
QY 353 ValAlaValThrLeuTyrGlyValAlaIleArgLeuThrValThrLeuPhePheProSerAla 372
DB 1753 GTGTCCCTAGCCCTTTCAATATCTTGGCTTCCACTCAACATC---CTGCCCATGGT 1809
QY 373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 392
DB 1810 ATCAGACAGATTGTGACAGGCGGAGCTGTCCCAAGCGTCAAGGATTTTCTGTCTCAT 1869
QY 393 AspGluIle-----SerGlnArgAsnArgGlnLeuProSerAspGlyIysIysMet 409
DB 1870 GAGGAGCTGAGCCAGACAGCATTTGAGCGAGGTGATCAAGATGAGAAAGGAATAGC 1929

Db 4045 ATCATTTGAGGGGTCAACATGCCCAAGATGGCGCTGCACAACTGGCTTCAAGATCAC 4104
 Qy 1119 ILeIleProGIngluProValIleuPheThrGlyThrMetArgLysAsnLeuAspProPhe 1138
 Db 4105 ATCATTCACAGGATCCGTGTTTGTTCCTCGGGGTTCCTCCGATGAACCTTGACCTTTT 4164
 Qy 1139 AsnGluHsrThrAspGluGluLeuThrPheAsnAlaLeuGlnGluValGlnLeuLysGluThr 1158
 Db 4165 AGTCAGTATTCAGATGAAGAAGCTCGATGAGCCCTGGAACCTTGCTCACTTAAGGCTTT 4224
 Qy 1159 ILeGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSer 1178
 Db 4225 GTGTACGCTTTCCTGCACAGCTGAACCATGAGTGTGCAAGAGGTGAGAGAACCTGAGT 4284
 Qy 1179 ValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeu 1198
 Db 4285 GTGGGGACGACGACACTGCTGTGCTGCGCCGGGGCTGTGCTGAGAGAAAGCAAGATTCTA 4344
 Qy 1199 ILeIleAspGluAlaThrLAsnValAspProArgThrAspGluLeuIleGlnLysLys 1218
 Db 4345 GTTTGTGACGAGGCTTACCGCACTGCTGACCTTGAAGACAGATTAACCTTTTCCAGTCCACC 4404
 Qy 1219 ILeArgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIle 1238
 Db 4405 ATCCGACGCACTTGTGAAGACTGTACTGTCTCAGATTGCTCATGCGCTTACACACATA 4464
 Qy 1239 ILeAspSerAspLysIleMetValLeuAspSerGlyArgLysLysGluLysArgGluPro 1258
 Db 4465 ATGCACTACACACGGGTTATTTCTCGTGCACAAAGAGAAAGATTCCGGAAGTGTGTGACCC 4524
 Qy 1259 TyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGly 1277
 Db 4525 TCTGAGCTCTGCAACAAAGA---GGCATCTTCTACAGCATGCGCAAGATGCTGCG 4578
 RESULT 11
 US-11-045-578-1
 ; Sequence 1, Application US/11045578
 ; Publication No. US2006024685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HO, Rodney J.Y.
 ; APPLICANT: YANG, Ziping
 ; APPLICANT: SHEN, Danny D.
 ; APPLICANT: WU, Daniel
 ; TITLE OF INVENTION: NOVEL SEQUENCE VARIANTS OF MULTI-DRUG RESISTANCE GENES, MDRI AND
 ; TITLE OF INVENTION: MRPI, AND RECOMBINANT CELLS EXPRESSING MRPI AND MDRI FOR
 ; FILE REFERENCE: 016336-002510US
 ; CURRENT APPLICATION NUMBER: US/11/045,578
 ; CURRENT FILING DATE: 2005-01-26
 ; PRIOR APPLICATION NUMBER: US 60/539,362
 ; PRIOR FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1
 ; LENGTH: 4599
 ; TYPE: DNA
 ; ORGANISM: rat
 US-11-045-578-1
 Alignment Scores:
 Pred. No.: 1,87e-204 Length: 4599
 Score: 2235.00 Matches: 493
 Percent Similarity: 57.2% Conservative: 288
 Best Local Similarity: 36.1% Mismatches: 463
 Query Match: 32.9% Indels: 122
 DB: 12 Gaps: 26
 US-09-976-858-42 (1-1325) x US-11-045-578-1 (1-4599)
 Qy 3 ProValTyrGlnGluVal-----LysProAsnProLeuGlnAsp-----AlaAsnLeu 18
 Db 586 CCCTGTCTCTGAAACTGTCCGTGACCCGAATCCATGTCCCAAGATCGAGTGTCTTTT 645

QY	19	CysSerArgValPhePheTrpTPrPLeuAsnProLeuPheLysIleGlyValSerArgArg	38
Db	646	CTTTCAGAGACACTCTTTTGGTGATTACAGGAGTGTGTGTCAGGGCTTACCGCACCC	705
QY	39	LeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlu	58
Db	706	CTGAAGACAGTAGACCTCTGTCTATTGAATTAAGAGAGACAGCTCAGAAAGATGGTACCT	765
QY	59	GluLeuGlnGlyPheTrpAspLysGlu-----	67
Db	766	GTGCTGGTGAATATCTGGAAGAGGAATGTGTTAAGTCGAGAGACAGCCTGACGATT	825
QY	67	-----	67
Db	826	GTGTATGCCCCCTCCAAAGATCCACCAAGCCTTAAGGAAGTTCTCAGTTGATGTGAAT	885
QY	68	-----ValLeuArgAlaGluAspAspAlaGluLysProSerLeuThr	81
Db	886	GAGGAAGTGGAGGACATGATTTGTCAAGTCAATCCACAAAGACCGGAGCCCTCTGTCTTC	945
QY	82	ArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIle	101
Db	946	AAGGTGGTGAACAGACCTTTGGCCCTTACTCTCTTCAAGAGCTCCGTGCAAGACCTT	1005
QY	102	GluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGlu	121
Db	1006	CATGACCTGATGATGTTGCTGGCCCTGAGATCTTGAAATGTGATATCAACTTCGTGAAT	1065
QY	122	AsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeu	141
Db	1066	GACAGGAGGAGCCCTGACTGG-----CAGGGCTACTGTGACAGACACTGCTG	1113
QY	142	ThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGlnCys	161
Db	1114	TTTGTCAAGTGCCTGTGACAGACACTGACACTCCACAGATCTTCATATCTGCTTCGTC	1173
QY	162	AlaGluMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysValAlaLeuArgLeu	181
Db	1174	ACCGGACATGGCATCAACAGACTGCTGTGTGGGGCGCTGTTACCGCAAGCTCTTGTGATC	1233
QY	182	SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuSerAsnAsp	201
Db	1234	ACCAATTCAAGTGAAGAAATGCTGCACAGCTTGAGAGATGTGTCAACCTCATGTCGCTGAT	1293
QY	202	ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTyrAlaGlyProLeuGln	221
Db	1294	GCCAGGAGCTTCATGACTGTGGCCACGTAATATTAACATGATCTGTGATGCCCTCTGCA	1353
QY	222	AlaIleAlaValThrAlaLeuLeuTyrPheGluIleGlyLysSerCysLeuAlaGlyMet	241
Db	1354	GTCAACCTAGCCCTTACTTCTGTGTGGCTGAACCTGGCCCTTGTGCTGTGGCGGGCTG	1413
QY	242	AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu	261
Db	1414	GCTGTATGATCCTCATAGTGCCCTTCAATGCTGTG-----ATG	1452
QY	262	ArgSerLysThrAlaThrPhe-----ThrAspAlaArgIleArg	274
Db	1453	GCCATGAAGACCAAGACTTACACAGTGGCACACATGAAGACCAAGAACCGAATCAAG	1512
QY	275	ThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTyrGluLysSer	294
Db	1513	CTGATGAACGAGATCTCTCAATGGGATCAAGTACTCAATTTGTACGGCTGGAGCTGGCT	1572
QY	295	PheSerAsnLeuIleThrAsnLeuArgLysGlyGluIleSerLysValIleLeuArgSerSer	314
Db	1573	TTCACAGCAAAAGTTATGACATCATCAGGACGAGGAGCTGAAGGCTGAAGAAATCCGCC	1632
QY	315	CysLeuLysGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheVal	334
Db	1633	TACCTGGCGGCTGGGACATTCACATGAGGTTTGCACACCTTCTCGTGGCTCTGTCA	1692

QY 335 ThrPheThrThrValLeuLeuGly-----SerValIleThrAlaSerArgValPhe 352
 DB 1693 ACCTTGGCTGCTTTGTGACTGTGACGAGGAAGAACATCTTGAAGCAAGAAACCTTT 1752
 QY 353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
 DB 1753 GATATCCCTGACCTGTTCAATATCTTGCCGCTTCCCACTCAACATC---CTACCCATGCTC 1809
 QY 373 IleGluArgValSerGluAlaIleValSerIleArgValGlyIleGlnThrPheLeuLeu 392
 DB 1810 ATCAGACAGATGTGACGAGCCGAGCGGTGCTTCAAGCGCTGAGATCTTGTGCTCAC 1869
 QY 393 AspGluIleSer-----GlnArgAsnArgGlnLeuProSerAspGlyLeuLys 408
 DB 1870 GAGGAGCTGTGACCCAGACAGCATTCAGCATGTGATGAAGATGTGTGAGGAGCATGAT 1929
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 DB 1930 AGCATCACTGTGAAGAAATGCAACTTCACTGGGCGAGG---GATGAACCTCCACACTG 1986
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 DB 1987 AATGCAATCACTTGTGCGCATCCCTGATGAGGCTTGTGCGGTGTGGCGAGGTAGGC 2046
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 QY 469 ValSerValIleGlyAlaArgIleAlaTyrValSerGlnGlnProTyrValPheSerGlyThr 488
 DB 2107 GTGACTGTCAAGGGCTCCGCTGCTATGTCGCCAGACGCTGTGATTCAGAAATGACTCT 2166
 QY 489 LeuArgSerAsnIleLeuPheGlyLysValTyrGlyLysGluArgTyrGlyLysValIle 508
 DB 2167 CTCCAGAGAAACATATCTGTTGGGGCGCCCTCGAGCAACATTCGTACAAAGCGGTGATG 2226
 QY 509 LysValaCysAlaLeuLysValAspLeuGlnLeuGluAspGlyAspLeuThrValIle 528
 DB 2227 GAGGCTGTGCTCTCTCCGATTTGGAAATCTCTCCAGTGGGAGCTTCACAGAGATT 2286
 QY 529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysValaArgValAsnLeuAlaArgAla 548
 DB 2287 GGTGAAGAGGTGTGAACCTGTGCGGGGGGCGAGAGACGCTGTGAGCTGTGCTGGGCT 2346
 QY 549 ValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValaAspAlaGlu 568
 DB 2347 GTGTATTGTAATCTGACATCTTACCTTGTGAGCAACCCCTCTCGAGCTGTGATGCACAT 2406
 QY 569 ValSerArgHisLeuPheGluLeuCysIle-----CysGlnIleLeuHisGluLysIle 586
 DB 2407 GTTGGAGACACATCTTGAAGAGGTGTGGGCTCCATGGGCTTACTGAAGAACAGACA 2466
 QY 587 ThrIleLeuValThrHisGlnLeuGlnIleTyrLeuLysAlaAlaSerGlnIleLeuLeu 606
 DB 2467 CGGATCCGTGTGACCCATGATGATACGTAACCTGCCCAAGATGATGATCATTTGTCAATG 2526
 QY 607 LysAspGlyLysMetValGlnLysGlyTyrTyrGlnPheLeuLysSerGlyIleAsp 626
 DB 2527 AGTGGCGGAGATCTCAGAGATGGATCTTATCAGAGCTCTTACGCGGATGGGCGGC 2586
 QY 627 PheGly-----SerLeuLeuLysValAspAsn 635
 DB 2587 TTTGCTGAGTTGTGGGACCTATGCAACCTAGACAGGACCTGCTTCAAGAGATGAC 2646
 QY 636 GluGlnSer-----GluGlnProProValPro----- 644
 DB 2647 AGTAAGAAATGTGTGAGTGTTTAGGAAAGAGTCAAAAGCGGTGAAAAAATGGATATCTG 2706
 QY 645 -----GlyThrProThrLeuArg-----AsnArgThrPheSerGlyLeu 657
 DB 2707 GTGACAGACGAGTGGAGAGCCCTGTGACAGGACATCTCAGCAACTCTTCTTCCACAGT 2766
 QY 658 SerValTyrSerGlnGln-----SerSerArgProSerLeuLysAspGlyValaLeuGlnSer 676

DB 2767 GTGCTTACTAACCGACAGACAGACAGCCGAGCTGTGAGAAAGTGTGGGTTAAAGAG 2826
 QY 677 GlnAspThrGluAsnValProValThrLeuSerGlyGluAsnArgSerGlu-----GlyLys 695
 DB 2827 GAGACTTGGAG-----CTGTGAGAGGACAGCAAGGCCCAACAGGCGAG 2871
 QY 696 ValGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAlaIleTyrIleValPhe--- 714
 DB 2872 GTGAAGCTTCCGCTGATGTGAATCTACATGAAGCCATGTGGCTGTGATCTCTCTTG 2931
 QY 715 ---IlePheLeuIleLeuLeuAsnThrAlaAlaGlnValaTyrValLeuGlnAspTyr 733
 DB 2932 AGTATCTTCTTTCCTGTGCAT-----CATGATGTGCACCTGCTTCAACAT 2982
 QY 734 TyrLeuSerTyrTyrAlaAsnLysGlnSerMetLeuAsnValThrValaAsnGlyGly 753
 DB 2983 TGGCTGACTCTTGTGACAGATGACCGCTGTGCAATGGAGACTCAGAG----- 3033
 QY 754 AsnValThrGluLysValAspLeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrVal 773
 DB 3034 AACAGAAATTTTCCAGCTAAGTCTATGTGGGCTTGGGCACTTGGCAAGGTGTGCACTA 3093
 QY 774 AlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPheTyrValaLeuValaAsnSer 793
 DB 3094 -----TTGGCTATTCATGGCTGTGTCCATTTGGGGGATCTT-----GCC 3135
 QY 794 SerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysValaProValLeuPhePhe 813
 DB 3136 TCCCGTCCCTGACACTGATGACCTGTACAGAAATGCTCCGACATGCCATGAGTTTCTTT 3195
 QY 814 AspArgAsnProIleGlyAlaArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAsp 833
 DB 3196 GAGGTACACCAAGTGGAGACCTAGTGAACGATTTCTCAAGAGTTGAGACAGCTGAGAC 3255
 QY 834 AspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValaGlyVal 853
 DB 3256 TCCATGATCCGCGAGGTATGAAGATGATTCATGGGTTCACTTCAAGTATGATGAGACT 3315
 QY 854 ValSerValaValaAlaValaIleProTyrIleAlaIleProLeuValaProLeuGlyIle 873
 DB 3316 GTCATCATCATCTTACCTGCTTACGCTTACGCTCCGACATCATCTCCACCTGTGGGCTG 3375
 QY 874 IlePheIlePheLeuAspArgTyrThrLeuGlnThrSerArgAspValaLysArgGln 893
 DB 3376 GTTATCTTGTGCAAGGATGTATGTGGCTCTCTTCAAGCTGAAGCGCTGAG 3435
 QY 894 SerThrThrArgSerProValPheSerHisLeuSerSerLeuGlnGlyLeuTyrThr 913
 DB 3436 TCTGTCACTGCTTCCCTGTGTACTACACTTTCATGAAGACTTGTGGGGGTCAAGTGC 3495
 QY 914 IleArgAlaTyrLysValaGlnGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeu 933
 DB 3496 ATCCGTGCTTGAAGAACAGAGGGCTTCAATGCGCAAAAGTACCTGAAGATGATGAG 3555
 QY 934 HisSerGluAlaTyrPheLeuPheLeuThrThrSerArgTyrPheAlaValaArgLeuAsp 953
 DB 3556 AACCAAGAGGCTTACCTACCCAGATGTGGCAACAGAGTGTGCTGTGCGCTGAG 3615
 QY 954 AlaIleCysAlaMetPheValIleIleValaIlePheGlySerLeuIleValaLysThr 973
 DB 3616 TGTGTGGCACTGATGTGTCTGTGCTGCTTGTGCGAGTCACTTCCCGGATATGC 3675
 QY 974 LeuAspAlaGlyGlnValaGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPhe 993
 DB 3676 CTCACTGTGCTGTGTGTGGCTGTCTGTGTGTCTTCACTCAGCAGATAGATGATCTTGT 3735
 QY 994 GlnTyrCysValaArgGlnSerAlaGlnValaGluAsnMetIleSerValaGluArgVal 1013
 DB 3736 AACTGTGATGTGAAATGCTCTGAGATGAGAACCAACATTTGGGAGTGAAGACTG 3795
 QY 1014 IleGluTyrThrAspLeuGluLysGluAlaProTyrGlnTyrGlnLysArgProProPro 1033

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Db      3796 AAGAAATATTTGAAACGAGAGAGGCTTCTTGCAAAATCCAAAGACAGCTCCACC 3855
      1034 Ala---TTPProHiegluYValIleIlePheAspAsnValAsnPhMetYrSerPro 1052
      3856 AACACCTGGCCCCATTCAGGCGGTGAGAGTTCCGGGATTACTGCTTGAGGTAAGAGAA 3915
      1053 GtlyGlyProLeuValIleuYshIleuThraIaleuIleLysSerGlnGluYValGly 1072
      3916 GACTTGACCTGGTTCTCAAGACACATAAATGTCAACCATGAGGGGTGAGAAAGGTTGGT 3975
      1073 ILeValGtYrThrgtYValIleGlyLysSerSerIleuIleSerAlaleuPheArgLeuSer 1092
      3976 ATTGTGGGTGTACAGAGCTGGAAATATCTTCAACCTGGGTTGTTCCGAAATCAAT 4035
      1093 Glu---ProGluGlyLysIleTTPleAspLysIleLeuThrGluIleGlyLeuHis 1111
      4036 GAGTCGACAGAGGAGAGATCATCATGATGGATTAACATGCTTAAGTTGGCTCGCAC 4095
      1112 AspLeuArgLysLeuMetSerIleIleProGlnGluProValLeuPheThrglyThrMet 1131
      4096 AACCTGGCTTCAAGATCAACATCATTCACAGAGATCTGTTTGTCCCGGGTTCCTTC 4155
      1132 ArgLysAspLeuAspProPheAsnGluIleThraAspGluGluLeuThraAsnIleGln 1151
      4156 CGCATGACCTGGACCTTTCAGTCAGTATCTGATGAAGAAAGTCTGGATGCTCGAG 4215
      1152 GluValIleGluYSerGluThrIleGluAspLeuProGlyLysMetAspThrgluLeuAla 1171
      4216 CTTCCTCACCTGAAGGGCTTTGTGTGAGCTTGTCCGACAGCTGAACATGATGTGGA 4275
      1172 GluSerGlySerAsnPheserValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIle 1191
      4276 GAAGGTGAGAGATCTGAGTGTGGGGCAGCAGACAGCTGTGTGCTGGCCGGCTTTGG 4335
      1192 LeuArgLysAsnGlnIleLeuIleIleAspGluAlaIleThraAsnValAspProArgThr 1211
      4336 CTGAGGAAACAAAGATTTCTAGGTGAGAGGCTGACAGAGCTGTGATCTGGAGAA 4395
      1212 AspGluLeuIleGlnIleLysIleArgGluYrPheAlaHisCysThraIleuThrIle 1231
      4396 GATGACCTTATTCAGTCCACCGTCCGAGAGAGCTTGAAGACAGTACTGCTCACTATT 4455
      1232 AlaHisArgLeuAsnThrIleIleAspSerAspLysIleMetValIleuAspSerGlyArg 1251
      4456 GCTCATCGGCTGAATACATATGACTATACAGAGGATGATGCTCTGGACAAAGAGAA 4515
      1252 LeuLysGluThraAspGluProGlyrValIleuLeuGlnAsnLysGluSerLeuPheYrLys 1271
      4516 ATTGGGAGGTGTGTGACCCCTCTGAGCTCTGCAAGAAAGA--GGCGTCTTCTATTAGC 4572
      1272 MetValGlnGlnLeuGly 1277
      4573 ATGGCCAAAGATGCTGGC 4590

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/ ORGANISM: Saccharomyces pastorianus
US-10-932-182A-484

Alignment Scores:
Pred. No.: 1,096-203 Length: 4551
Score: 2227.00 Matches: 499
Percent Similarity: 56.64 Conservative: 256
Best Local Similarity: 37.44 Mismatch: 497
Query Match: 32.84 Indels: 82
DB: 7 Gaps: 23

US-09-976-858-42 (1-1325) x US-10-932-182A-484 (1-4551)

      4 ValTyrGlnGluVal-----LysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
      598 ATACATCAGAAAGTGTATGAGAAAGAAACCGAACCCGTGATGAGCTTAATATATTCCTCC 657
      21 ArgValIlePheTTPleuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
      658 AGAATTACATTTTCTTGATGTCAAGTTTAATGAAMACTGGATATGAATAAATACCTGATA 717
      41 GluAspAspMetYrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
      718 GAGCTGATTTGTATTAATTAACAAAAAATTAGTACAGACAGAACTCTCAGAAATTA 777
      61 GlnGlyPheTTPAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
      778 GAGAAATAATGGCAAAATGAAGACTT-----AAGCATAAATCAAAACCTTCCTTA 825
      81 ThraGlnAlaIleIleLysCysTyrTTPlysSerYrLeuValIleGlyIlePheThrLeu 100
      826 TCTTGCGCTAATATGCAAAACTTTTGATATTAATAATGTTTAGCCGCTTCTCAAAAGCC 885
      101 ILeGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnYrPhe 120
      886 ATTATGATATTTCTGGCATTTGTGTGCAACACACATTAACAAATTTTAATCAAGTTGTT 945
      121 GluAsnYr-----AspProMet-----Asp 127
      946 ACCGACTCAATTAAGAAAGCAAGATGATGACATCTTAACTCTGCGATATGTGAT 1005
      128 SerValAlaLeuAsnThraIleYrAlaYrAlaThraValIleuThrPheCysThrLeuIle 147
      1006 AAGCTGTGACAAAAATTCGCCATTAAGAGGTTTAAGATGGCTTTTCCATGTTCTTG 1065
      148 LeuAlaIleLeuHis-----HisLeuYrPheYrHisIleValGlnCysAlaGly 163
      1066 GTTGGGTTTACTCAAAACATCTGTGTGATCAATATTTTGAATGTCTTAAACAGTGT 1125
      164 MetArgLeuArgValAlaMetCysHisMetIleYrArgLysAlaLeuArgLeuSerAsn 183
      1126 ATGTATGTCAAAAGGCTTGATGCTGCTGATATACCAAAAGGCTTGTATTTATCTAAT 1185
      184 MetAlaMetGlyLysThrThrglyGlnIleValAsnLeuLeuSerAsnAspValAsn 203
      1186 GAAGATCTGACCTTCACTTACTGTGACATCGTTAATTAATGAAGGTGAGTGTCCAA 1245
      204 LysPheAspGlnValThraValPheLeuHisPheLeuThraGlyProLeuGlnAlaIle 223
      1246 AAATTACAAAGATCTACTCAATGTTAAATTTGATTTGTGTCAAGGCTTTCAGATTAAT 1305
      224 AlaValThraIleLeuTTPMetGluIleGlyLysSerCysLeuAlaGlyMetAlaVal 243
      1306 ATCTGTCTTACTCTTTGATTAAGCTAATTTGGTAAATTCAGATGGGTTGATATCATTA 1365
      244 LeuIleIleLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSer 263
      1366 CTAGTTGTTAAGATGCCATTAATTCATTTTAATGAATAACAAAGAAATTAACAAA 1425
      264 LysThraIleThraPheThraAspAlaArgIleArgThrMetAsnGluValIleThrglyIle 283
      1426 TCTCAATGAATATACAAAGAGAAAGAACTGTGTATTAAGTGAATTTCTAAACAACATC 1485

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Db      3592 TTCAGCTAAAGCAAGTACTTGACGCGGCTGATGCTTGTGCTGCTAAAGTATGCA 3651
Qy      987  LeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsnMet 1006
Db      3652 TTACAAATGACCCAAACATTGATGATTTAGATGATGACGTTGATGATGAAACCAT 3711
Qy      1007 MetIleSerValGluArgValIleGluTrpThrAspLeuGluLeuAspProTrpGlu 1026
Db      3712 ATGTGTCGCTGAGGAAATTAAGAAATGCGTACGCTTAAGAGTACGCGCTTAACTT 3771
Qy      1027 TyrGln---LysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
Db      3772 ATCGAAGCTACAGGCGCCACCAAGATGCGCAGGCGCAAGTACATCAAGTTCATCA 3831
Qy      1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
Db      3832 TATTCACCTCGTTATGACCAAGCTTGATCTTGTCTGTAACAGATTGATATTCATC 3891
Qy      1066 LysSerGlnGluLysValGlyIleValGlyArgTrpGlyValAspLysSerSerLeuIle 1085
Db      3892 AAACCCGAGGAAAAAATGCTATTTGTTGTAAGAACAGGTCAGTAAATCGTCTTAA 3951
Qy      1086 SerAlaLeuPheArgLeuSerGluProGlu---GlyValIleTrpIleAspLysIleLeu 1104
Db      3952 TTAGCGCTATTCGAATCATTTGAAGCTAGTCCGCGAAATATTTGTTATGATGACAT 4011
Qy      1105 ThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluPro 1124
Db      4012 ATTAATGAATATGCGTTATATGATGATTAAGACATTAACCTGCTCAATTAATCTCAAG 4071
Qy      1125 ValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisIleThrAspGlu 1144
Db      4072 CAAGTGTGTAAGGTACTGTTGCTGAGAAATATGATCAATCAACCAATACCAATGAG 4131
Qy      1145 GluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGly 1164
Db      4132 GCTATGTGAGAGCATTTGAACTTTCTCATTTGAAAAAACAATGTTTCAATGAGTAA 4191
Qy      1165 Lys---MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGln 1183
Db      4192 GATGGTTAGACTCTCAATTAATACAGAAAGGTGGTAGTAACTTAAGTGTGGACCAAGACA 4251
Qy      1184 LeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAla 1203
Db      4252 TTAAGTGTCTGCGAGACCAATGCTGTTCCATCCAAATTTTGGTGTAGTGAAGCC 4311
Qy      1204 ThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPhe 1223
Db      4312 ACCGCTGACGTGATGTCGAAACAGATAGATCATTCAGAGACATATGCGACGCGCTTT 4371
Qy      1224 AlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys 1243
Db      4372 AGAGATGAGAACTATTTGACTATTCGACACAGGTTGAACACATTCAGATGACGATTA 4431
Qy      1244 IleMetValLeuAspSerGlyArgLeuLysGluTrpAspGluProTrpValLeuGln 1263
Db      4432 ATCATGTGTTGGATACGTAACGTAAGTGGCTGATTTGATTTCCCAATCCACGCTATTA 4491
Qy      1264 AsnLysGluSerLeuPheTrpLysMetValGlnGlnLeuGly 1277
Db      4492 AATACCAAAATCATTTATTTCTATTGTTGTCACGGAAGCCGGT 4533

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RESULT 13

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US-10-932-182A-484
; Sequence 484, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIMIZU, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

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; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 484
; LENGTH: 4551
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-484

Alignment Scores:
Pred. No.: 1,09e-203 Length: 4551
Score: 2227.00 Matches: 499
Percent Similarity: 56.64 Conservative: 256
Best Local Similarity: 37.48 Mismatches: 497
Query Match: 32.84 Indels: 82
DB: Gaps: 23

US-09-976-858-42 (1-1325) x US-10-932-182A-484 (1-4551)
Qy      4 ValTyrGlnGluVal-----LysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
Db      598 ATACATCGAAAGTTATGAGAAAGCAACCGCTACGATAGTGTATATATATCTCC 657
Qy      21 ArgValPhePheTrpIleuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
Db      658 AGAATTAACATTTCTTGATGATGACGTTTAAATGAAACCTGATATGAAATACTAGTA 717
Qy      41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
Db      718 GAAAGCTGATTTGTATTAATTTACCAAAAACTTATGACACAGAACTCTTCAGAAATTA 777
Qy      61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
Db      778 GAGAAAAATTTGGCAAAATGAACTT-----AAGCATTAATCAAAAGCTTCGTTA 825
Qy      81 ThrArgAlaIleIleLysCysTrpTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
Db      826 TCTTGCGCTATATGCAAAACCTTTGATATTAATATGTTTAAAGCCGCTTCGAAAGCC 885
Qy      101 IleGluLysSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTrpPhe 120
Db      886 ATTCATGATATTTCTGCGATTCGTCGACCAACATTAATTAATTAATCAAGTTGTT 945
Qy      121 GluAsnTrp-----AspPromet-----Asp 127
Db      946 ACCGCTGACATTAAGAAAGACAGATGATGACGATCTTTAACTCTCGGATATGCTGAT 1005
Qy      128 SerValAlaLeuAsnThrAlaTyrAlaThrValLeuThrPheCysThrLeuIle 147
Db      1006 AAGCTGATCAAAATTTGCCATTTAAGAGTTTATGATGCTTTTCCATGTTCTTG 1065
Qy      148 LeuAlaIleLeuHis-----HisLeuTrpPheTrpHisValGlnCysAlaGly 163
Db      1066 GTTGGTTTACTCAAAACATCTGTGCTGCATCAAAATTTTGAATGATCTTTAAACACTG 1125
Qy      164 MetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsn 183
Db      1126 ATGTATGTCAAAGTGCCTTGAATGCTGATGATTAACAAAGGCTTTGATTTATCTAT 1185
Qy      184 MetAlaMetGlyLysThrThrThrGlnGlnIleValAlaAsnLeuLeuSerAsnAspValAsn 203
Db      1186 GAAAGCATCTGACCTTCACTTACTGCTGACATCGTATTTATTAATGAGGTGATGCCAA 1245
Qy      204 LysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIle 223
Db      1246 AAATTACAAAGATCTGACCAATGTTAATTTGATTTGATTTGTCAGGCGCTTCAGATTAT 1305
Qy      224 AlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaVal 243
Db      1306 ATCTGCTCTACTCTTGTATTAAGCTATTTGGGTATTAATGATGCTGGTGGTGTATCAT 1365

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244 LeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSer 263
 1366 CTAGTTGTTATGATGCTAATTAATTTTAAATGAGAAATCAAAAGAAATTAACAAA 1425
 284 LysThrIleAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIle 283
 1426 TCTCAAAATGAAATACAAAGACAAAGAAAGAACTGCTGTTATTAAGTAAATTCAAACAAATC 1485
 284 ArgIleIleLysMetCysThrAlaTrpGlyLysSerPheSerAsnLeuIleThrAsnLeuArg 303
 1466 AATCTCTGAAATTTATATCCGCGGAAAGACCTTACAGGAGAAAGTGGAAACGCTTACA 1545
 304 --LysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAla 322
 1546 AATAACAAAGAACTAATTAATTAATTAATGAGTGTATATGAGTGTATATGAGTGTAT 1605
 323 SerPhePheSerAlaSerLysIleIleValIlePheValIleThrPheThrThrTyValLeuLeu 342
 1606 CAATTTAATCATGATTCCTTCTTCTAGTTCATGCTGACCTGCTGCTGCTGCTGCTGCTG 1665
 343 ---GlySerValIleThrAlaSerArgValIlePheAlaIleValIleThrLeuTyGlyAlaVal 361
 1666 GAAGATGAGGCTTGAATCAACCAATGATTTTCTGCTTAACTCTTTTCAATCTTACT 1725
 362 ArgLeuThrValThrLeuPhePhePheProSerAlaIleGluArgValSerGluAlaIleVal 381
 1726 TCATTTCCATTG---ATGATTTATTCACATGCTTTGAATTCATTTATCAACACTCTGTT 1782
 382 SerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSer-----Gln 397
 1783 TCTATTTGAGAGCTTATTTCTTTTTCACATGAGAGCTACAGCAGATTCCTGTTGACG 1842
 398 ArgAsnArgGlnLeuProSerAspGlyLysLysMetValHisVal---GlnAspPheThr 416
 1843 CGCTTACCAAAAGTGAATATGTTGCTGATATAGCATCAATATTTGGCAGACACCTTAC 1902
 417 AlaPheTrpAspLysAlaSerGlu---ThrProThrLeuGlnGlyLeuSerPheThrVal 435
 1903 TTTTATGCGCAACGTAACCAAGATTAATTAAGATGCGTTGAAAAATATCAATTTCCAGCT 1962
 436 ArgProGlyGluLeuLeuAlaValAlaGlyProValIleGlyAlaGlyLysSerSerLeuLeu 455
 1963 AAGAAAGGAGATTAACCTGATTTGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGT 2022
 456 SerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIle 475
 2023 TCACACCAATTTGGGAGCTTATTTAGAGTCAAAAGGGTTTGGCTGACGCTGATGCT 2082
 476 AlaTyValSerGlnProTrpValIlePheSerGlyThrLeuArgSerAsnIleLeuPhe 495
 2083 GCATTCGCTCTCAAGGTTCCATGATTAATGAATGGAGCGGTCAAGGAAACATTTTGT 2142
 496 GlyLysLysTyGluLysGluArgTyGlyGlyValIleLysAlaCysAlaLeuLysLys 515
 2143 GGGGCAATGATGAGTGCATTTTATGAAAAAATCATCAAGCGCTGCTGTTAACCAT 2202
 516 AspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeu 535
 2203 GACTTGGCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2262
 536 SerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaValTyGlnAspAlaAspIle 555
 2263 TCGGGCGGCAAAAGGACGCTTATCTTACGAAAGGAGCTTATTCAGAGGCGAGACT 2322
 556 TyLeuLeuAspAspProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGln 575
 2323 TATCTACTGAGACGATCCCTTGGCGGCTGTGAAGAAACAGTGGCTAGCATTTGGTCAA 2382
 576 LeuCysIleCysGln-----IleLeuHisGlyLysIleThrIleLeuValThrIleGln 593
 2383 CATGTAATGGGTCAAAATGTTACTACTACTCAAAACCAAGTTATTTGGCAACGAAACAA 2442
 594 LeuGlnTyLeuLysAlaAlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGln 613

2443 GTAAAGCGCTTATCTGTTGACAGATTCATTTGATTAATTAATGAATGAATTAATTTCA 2502
 614 LysGlyThrTyThrGluPheLeuLysSerGly-----Ile 625
 2503 CAAGGACATATGATGATTAATTAACCAAGACCGGACCTCTCCCTTGGAAATTAATCAAC 2562
 626 AspPheGlySerLeuLeuLysLysAspAsnGluGlnSerGluGlnProProValProGly 645
 2563 GATTATGCT-----AAAAACAAATATATACACAGAGGAAACAGTGAATCTTCA 2613
 646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnIleSerSer 665
 2614 ACTAATCAATTCGGGAAACAGTATACCGATTGAGGCGAGCTGGAACATTAACAAA 2673
 666 ArgProSerLeuLysAspGlyAlaLeuLysSerGln----- 677
 2674 CTAAATGATCTGATTTGCGCAACGCTACACTCAAGCTTAAGAAAGCTATGATGCA 2733
 678 -----AspThrGluAsnValProValThrLeuSerGluGln 689
 2734 ACTTACCGCAGTATGATTTTGGCATGATGAAACGTT-----GCTAAAGAGA 2784
 690 AsnArgSerGluGlyLysValGlyPheGlnAlaTyLysAsnTyPheArgAlaGlyAla 709
 2785 CATCGTGAACAGGGAGAGTGAAGTGAACATTTACTACAGATGACGCTAAACCTTGTAC 2844
 710 HisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGlnAlaTyVal 729
 2845 CCAAAAGCTGTTGTGTCTCATATATGTTTTC---GTTATATCAATGTTCTTATCCGCT 2901
 720 LeuGlnAspTrpTrpLeuSerTyTrpAlaAsnLysGlnSerMetLeuAsnValThrVal 749
 2902 ATGGGTACGTTTGTGTTGAACACCTGTCCTCAAGTTAATGCGCTATGCGGCTATCCG 2961
 750 AsnGlyGlyGlyAsnValThrGluLysLeuAsnTrpTyLeuGlyIleTySer 769
 2962 AATGCTGCTCGT-----TACTGGGATCTATATTC 2991
 770 GlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuValPhe---Ty 788
 2992 GCCCTGTGATTTGTTGACCGCTGCAACTTAATTAATGACATTTTGGTGGTCTAC 3051
 789 ValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysAla 808
 3052 TGCATTAATCAAGCTCCCAATATTTGCAACATTTGATGACAACTCTGCTGAAGAGCT 3111
 809 ProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAsp 828
 3112 CCAATGACCTTTTTCGAACCAACACACCGATTTGTGATAATTTTAAACGTTTTTGAATGAT 3171
 829 IleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeu 848
 3172 ATATATTAAGTTGATGCTTTTGGGAGAAACCTTTTCTCACTTTTGTGTAATCGGTA 3231
 849 GlnValValGlyValValSerValAlaValAlaValIleProTrpIleAlaIleProLeu 868
 3232 AAAAGTTAGCTTACTATTAATCTGTTATTTGTGGACAAACGTTGCAATTTTATTAATC 3291
 869 ValProLeuGlyIleIlePheIlePheLeuArgArgTyPheLeuGluThrSerArgAsp 888
 3292 GTTCATTTGGGTGTGTTTACTTATCATTAATCAACAGTACTATTTTAAAGACATCAAGGAG 3351
 889 ValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSerSerLeu 908
 3352 TTGCGTCTGTTAGATTTATCAACAGGTCTCCAAATTTTCTCAATTTTCAAGAACTTTG 3411
 909 GlnGlyLeuTrpThrIleArgAlaTyTyLysAlaGluGluArgCysGlnGluLeuPheAsp 928
 3412 GCGGCTCTTCTACAGTTAGAGTTATTCACAGCAAAAGAGTTTTCACACATTAATCA 3471
 929 AlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPhe 948

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Db      3472 TGTGTTATGATTAATACATGAGTGGCTTTATCTCTGTCATAGCTAATCGTTGGTTG 3531
Oy      949 AAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeu 968
Db      3532 GCATACAGATTGGAACCTTATGTTCTGTATATTTTGGGGCGCTACTTATTCGGTT 3591
Oy      969 IleuAlaIys-----ThrIleuAspAlaGlyIleValIleGlyLeuAlaLeuSerTyra 986
Db      3592 TTCAGGCTTAAGCAAGAGTACCTTGACCTGGGCTATGCTGGTTGGTTCGCTAGTTATGCA 3651
Oy      987 LeuThrIleuMetGlyMetPheGlnTrpCysValArgIleSerAlaGluValAlaGluMet 1006
Db      3652 TTACAAATATACCCAAACATTGATTTGATTTGATGATGACCTTGAATGAGTGAACCAAT 3711
Oy      1007 MetIleSerValGluArgValIleGluTrpThrAspLeuGluIleGlyValAlaProTrpGlu 1026
Db      3712 ATGTGTTGGCTGAGAGATTTAAGATACGCTGACTTAAAGATGAGCGCCCTTAGTT 3771
Oy      1027 Tyrgln--LysArgProProProAlaTrpProHisGluValIleIlePheAspAsn 1045
Db      3772 ATCGAAGGTCAACAGGCGCAAGGATGCGCAGGCAAGGTGACATCAAGTTCAATCA 3831
Oy      1046 ValAsnMetCysSerProGlyGlyProLeuValIleuHisIleuThrAlaLeuIle 1065
Db      3832 TATTCCTACTGTTATGACCAAGCTTGATCTTGTCTGAAACAGATTGATATTCACATC 3891
Oy      1066 LysSerGlnGluIleValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
Db      3892 AAACCGAAGGAAAAATTGGTATTTGTTGTTAGAACAGGCGCAAGTAAATCGCTTTAA 3951
Oy      1086 SerAlaLeuPheArgLeuSerGluProGlu--GlyLysIleTrpIleAspLysIleLeu 1104
Db      3952 TTAGCGCTATTCAGATCATTTAGAGCTAGTGGCGGAAATATTGTTATGATGACATTC 4011
Oy      1105 ThrTrpGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnIlePro 1124
Db      4012 ATTAATGAATATGGGTTATATGACTTAAGACATTAACCTGCTCAATTAATCTCAAGATTC 4071
Oy      1125 ValIleuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisIleThrAspGlu 1144
Db      4072 CAAGCTTTGAAGAGTACTGTTCTGTAGATATCGATCCATCAACCAATACCCGATGAG 4131
Oy      1145 GluLeuTrpAsnAlaLeuGlnGluValGluLeuLysGluTrpIleGluAspLeuProGly 1164
Db      4132 GCTATGTGAGAGCATTTGGAATCTTCTCATTTGAAGAACATGTTATCATGAGTAAAC 4191
Oy      1165 Lys---MetAspThrGluLeuAlaGluSerGlySerAspPheSerValGlyIleArgGln 1183
Db      4192 GATGGGTATGACTCTCAATTAACAGAAAGGTGTAGTAACTTAAGTGTGGACAAAGACAA 4251
Oy      1184 LeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAla 1203
Db      4252 TTACGTCTGCTTCCAGAGCAATGCTGTTCCATCCAAATTTTGGTCTGATGATGAGCC 4311
Oy      1204 ThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPhe 1223
Db      4312 ACCGCTGACGTGATGTGCAAAACAGATAGATCATTCAGAGCAATTCGACGCGCTTT 4371
Oy      1224 AlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys 1243
Db      4372 AGAGATAGAATATATATGACTATCGACACAGAGTTGAACCACTCATGATGACCGATTA 4431
Oy      1244 IleMetValLeuAspSerGlyArgLeuLysGluTrpAspGluProTrpValIleuGln 1263
Db      4432 ATCATTTGTTGGATTAACGGTAAAGTGGCTGAGTTGATTTCCCATCCCACTATTAAAC 4491
Oy      1264 AsnLysGluSerLeuPheTrpLysMetValGlnGlnLeuGly 1277
Db      4492 AATACCAATCATTAATTCTATTGTTGTGACAGGAAGCGCGT 4533

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RESULT 14
 US-11-136-527-2145
 ; Sequence 2145, Application US/11136527

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; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2145
; LENGTH: 4954
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2145

Alignment Scores:
Pred. No.: 3,956-201 Length: 4954
Score: 2201.00 Matches: 495
Percent Similarity: 55.7% Conservative: 266
Best Local Similarity: 36.2% Mismatches: 478
Query Match: 32.4% Indels: 128
DB: 12 Gaps: 24

US-09-976-858-42 (1-1325) x US-11-136-527-2145 (1-4954)
Oy      12 ProLeuGlnAspAlaAsnLeuCysSerArgValPhePheTrpTrpLeuAsnProLeuPhe 31
Db      671 CCATGAGTCACGGCTTCTCTTCTGAGTACATTAATTAAGTGTATGACAGCTGTT 730
Oy      32 LysIleGlnLysLysArgArgLeuGluGluAspMetTySerValLeuProGluAsp 51
Db      731 CTGAAGGTTCAACACATCACTGACACTAGAAGATGCTGGGATATGATGAAGGTTT 790
Oy      52 ArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeuArgAla 71
Db      791 AAAACAGGTCACTCACAGCAAGTTTGAAGCGGCCATGACAAAGACCTTGCAAAAGCC 850
Oy      72 -----GluAsnAspAlaGlnLysProSerLeuThr----- 81
Db      851 AGCGAGGCTTTTCAGAGCGCGGCTGCAGAAATCCAGCGAAACCTTGAGCCACACTACAC 910
Oy      81 ----- 81
Db      911 GGACTGAACAAGAACAGACAGTCAAGCAAGCGTTCTGCTCGAAGAAAGCAAAAG 970
Oy      82 -----ArgAlaIleIleLysCysTyTrpLysSerTyLeuValLeuGlyIlePhe--- 98
Db      971 AAGTCTGAGAAAGCACCAACCAAGATATCCCAATGCTGTGATGATCAAGTCTCTTCAAA 1030
Oy      99 -----ThrIleuIleGluGluSerAlaLys 106
Db      1031 ACCTTCACGTAAGTATCTGAAATCATTTATGAAATTAATTAATCATGACCTTTGGTG 1090
Oy      107 ValIleGlnProIlePheLeuGlyLysIleIleAsnTyPheGluAsnTyAspProMet 126
Db      1091 TTTCTGAATCTCCACAGTGTGAAGTGTGATCGGTTTC----- 1129
Oy      127 AspSerValAlaLeuAsnThrAlaTyraTy-----AlaThrValLeuThr 142
Db      1130 -----GTGAAGAGCTTAACATCAATACGATGCTGTGGCTATATATGTCATTAATG 1183
Oy      143 PheCys---ThrIleuIleLeuAlaIleuHisIleuTyPheTyHisValGlnCys 161
Db      1184 TTTGTGTGACTCTATCCAAATCTTTGCTTGCCTTCACTTACTTCAACATGTTTGTG 1243
Oy      162 AlaGlyMetArgLeuArgValAlaIleMetCysHisMetIleTyArgLysAlaLeuArgLeu 181
Db      1244 TTGGGAATGTGGTATGCGAACAACCGTCATGTTTGTGATATATGAAGAGCAATGACCCCTA 1303
Oy      182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201

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QY      872  GilyllelePheleuargyrrhphleugluThrSerArgspVallylsarg 891
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3473  ACACATTCTTATATTTCGGTGCAGGTTTTTATATGTCGACTTCCGCGCAGCTGAGACGG 3532
QY      892  LeugJuserThrThArgserProvalPheSerHisleuSerSerleugluThy 911
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3533  TTGGATTCTGTGCACCAAACTCCGATCTTCTCATTGAGAGCTGTCAGAGTTTG 3592
QY      912  TPTThrleArgAlaTyrlsAlaglulugluArgCySgluInluPheaspAlahlgln 931
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3593  CCCATTATCCGTCCTTTCAGACACGACGCACTTTCAGCTTGGAAATAGAAAGCAGATT 3652
QY      932  AspleuHisSerGluAlaTrpPheleuPheleuThrThSerArgTrpPheAlaValarg 951
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3653  GACATCAACCAAGAAATGTCTTTCTTCGATTAACCTCCAAACGAGGTGCTCAATTGCG 3712
QY      952  LeuaspAlaIleCyAlaMetPheValIlelleValAlaPheGlySerleulleuAla 971
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3713  CTGGAGCTGGTTGGAACCTTGTCCTTCTGCTCGCTTCTGCTGCTGTTATTTATAGA 3772
QY      972  LysThrleuaspAlaglYgluValGlyleuAlaLeuSerTyrlaLeuThrleuMetGly 991
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3773  AAAACCTTAACCGGAGCAGCTGTGGCTTGTCTTCTCAACGCTTCAATTCACACAA 3832
QY      992  MetPheGlnTrpCyValargInseralaglValGluAspMetIleSerValGlu 1011
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3833  ACCTTGAACCTGGCTAGTGCAGATGACCTGAAAGCAGACCAACATTGTGGCAGTTGAG 3892
QY      1012  ArgValIleGluTyrlThraspleuGluYlsgluAlaProTrpGluTyrlGlnlysbatPro 1031
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3893  CCAATTAAGTAATACCTAATATAGAGATGAGGCCCTCGGTGTCAGCAAGGCGCT 3952
QY      1032  ProProAlaTrpProHisgluGlyValIlellePheaspAspValaAspMetTyrlSer 1051
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      3953  CCGGACGACTGGCCGACAGATGTGAGATTCAGTTTAACTATCAATGCGGATTCGG 4012
QY      1052  ProGlyGlyProleuValleuYsbHleuThralaLeuIleYsbSerGlnGluYsbVal 1071
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4013  CCGGAGCTGGATCTGGTACTGAAAGGATCATCTTGAACATCAAGAGCGGAGAAAGTC 4072
QY      1072  GlylleValGlyArgThrGlyAlaglYlserSerleulleSerAlaLeuPheargleu 1091
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4073  GGCRTTGTGGGSMGAGCTGGGCTGGGAATCATCCCTACRABSTGCTCTTCGAAATC 4132
QY      1092  SerGluProGlu---GlylYsbIleTrpIleAspYlIleuThrGluIleGlyleu 1110
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4133  TTAGAGCTCGCGGGGCGGACGATCATCATTTGATGGATGATGATGATGATGATGATG 4192
QY      1111  HisaspLeuArglylYsbMetSerIleleProGlnGluProValleuPheThrGlyThr 1130
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4193  CACGACCTTCGAGAGAGGCTGACATCATTCGCCAGAGCCCATTTGTTCTCGGGAGAT 4252
QY      1131  MetArglyAsnleuAspProPheAsnGluHisThraspGluGluLeuThrasnAlaLeu 1150
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4253  CTGAGGATGAATCTCAACCTTTTCACAAATATTCAGATGAGAGAGGTTGAGGGGCTCG 4312
QY      1151  GlnGluValGlnleuYsbGluThrlleGluAspLeuProGlylYsbMetAspThrGluLeu 1170
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4313  GAGTTGGCTCACTCGATTCCTTTGTGTCTGCGCTTACAGCTTGGGTGTTATCCGAAGTG 4372
QY      1171  AlaGlySerGlySerAspPheSerValGlylnArglnleuValCySerleuAlaArgAla 1190
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4373  ACAGAGGCTGTGCACAACTGAGCATAGGAGAGGCACTCTTATGCTCGGGCAGGGCT 4432
QY      1191  IleleuArglyAsnGlnIleleuIlelleAspGluAlaThralaAsnValaspproArg 1210
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4433  GTGCTTCGAAATCCCAAAATCTGTGCTCGATGAGAGCAACGCTCAGTGATCTCGAG 4492
QY      1211  ThraspGluLeuIleGlnlysbYlIeArgGluYsbPheAlaHisGlySerThralleuThr 1230
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4493  ACGGATGAGCTCATTCAGACGACCATCCAAAGAGATCTCCAGTGACGCGKCATCACC 4552

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QY      1231  IleAlaHisArgleuAsnThrIlelleAspSerAspYlIleMetValleuAspSerGly 1250
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4553  ATCCCTTCACAGGCTGCACACCATCATGACAGTGACAAAGATATGTCCTTACACACGG 4612
QY      1251  ArgleuYsbGluTyrlAspGluProGlyrValleuLeuGlnAlaMetYsbGluSerleuPheTyrl 1270
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4613  AAGATTGCGAGTATAGGACGTCCTCAAGAAATGCTGTCCAAACAGAGTTCC---TTCTAT 4669-
QY      1271  LysMetValGlnGlnleuGly 1277
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      4670  CTGATGGCCAAAGAACCGGCGC 4690

RESULT 15
US-11-136-527-475
; Sequence 475, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
; LENGTH: 5189
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-475

Alignment Scores:
Pred. No.: 1,76-198 Length: 5189
Score: 2174.00 Matches: 484
Percent Similarity: 56.18 Conservative: 277
Best Local Similarity: 35.78 Mismatches: 485
Query Match: 32.04 Indels: 110
DB: Gaps: 24

US-09-976-858-42 (1-1325) x US-11-136-527-475 (1-5189)
QY      3  ProValTyrlGlnGluValIlePheAspProleuGlnaAspAlaAsnCySerArgVal 22
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      658  CCAGAGAACTTGAACAAATCTTCCAGAGGCCAGCGCTGCTTCTTCTCCGCTCG 717
QY      23  PhePheTrpTrpPheAsnProleuPheYsbIleGlyHisYsbArgArgleuGlnuAsp 42
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      718  TCTTCTGCTGTGTTCACAAAGCTTGCATCTTGGCTTACCAAGCTCCCTGAGGACAGT 777
QY      43  AspMetTyrlSerValleuProGluAspArgSerGlnHisleuGlyGluLeuGlnGly 62
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      778  GACCTCTGTCTCTGTCTGAGAGGACTGCTCTCAAGAGTGCTTCAACGCTACTCGAA 837
QY      63  PheTrpAspYlsglu----- 67
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      838  GGATGCAAAAGACAGACAGCCAGCATAGGGCCCCAGACTGACGCTTGAAGCCAAAG 897
QY      68  -----ValleuArgAlagluaAspAlaGlnlyPheSerleu 80
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      898  ATCGAGGTGAGATGAGGTCTGCTGAAGGCCGCCCCMAAGACCAAGAACCTTCTTT 957
QY      81  ThrArgAlaIlelleYsbCyserTyrlTrpYsbSerTyrlleuValleuGlyllePheThrlleu 100
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      958  CTGAGGCTTGTGTAGAACCTTCACTTCACGCTTGTCTCATAGGGTCCCTTCAAGCTG 1017
QY      101  lleGlnJuserAlaIleValIleGlnProIlePheleuGlyYsbIleAsnTyrlPhe 120
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db      1018  ATCCAGACGCTGCTCTCTTATCAACCAACGATGCTGATGATCCTCATGAGTTTAT 1077
QY      121  GlnuAsnTyrlAspProMetAspSerValAlaLeuAsnThrAla-----Tyrl 135
      |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

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QY 806 LeuValAlaProValLeuPheAspArganProIleGlyArgIleLeuAsnArgPhe 825
 Db 3208 ATCCGGCCCTCATCTCTTTGGACACGACGCCCTTCAGCGCGCATCTCATCTGTTTC 3267
 QY 826 SerIlyAspIleGlyHisLeuAspArgLeuProLeuThrPheLeuAspHeileGln 845
 Db 3268 TCACAGACATATACCTCATCTGATGAGGTTCTGCCCCCACCACCATCTCATGCTTCAAT 3327
 QY 846 ThrLeuLeuGlnValValAlaValAlaValAlaValAlaValAlaValAlaValAla 865
 Db 3328 TCATTTACACATCCATCTCCACCATTTGGTATATGTTGTCAGCAGCAGCATCTTCTCC 3387
 QY 866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGlnThr 885
 Db 3388 GTGGTGTCTTCTCTGCTGCTGCTCATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 3447
 QY 886 SerArgAspValIlyArgLeuGlnSerThrThrArgSerProValPheSerHisLeuSer 905
 Db 3448 TCGAGCAGCTGAGAGACTGAGCTGATCCGTTAGCGGCTGCGCCCATCTTCCCATCTTCTG 3507
 QY 906 SerSerLeuGlnGlyLeuThrThrIleArgAlaIlyIlyAlaGlnGlnArgCysGlnGln 925
 Db 3508 GAGACAGTAACAGGACCCAGTGCATTCGGGCTTACGGCCGAGTCCACAGACTTCAAGTC 3567
 QY 926 LeuPheAspAlaHisGlnAspLeuHisSerGlnAlaIlePheLeuPheLeuThrThrSer 945
 Db 3568 CTCAGTATGCTTAAAGGTGATAGCAACAGAACCCATTCCTTACATCCCTCCAC 3627
 QY 946 ArgThrPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleValAlaPhe 965
 Db 3628 CGGTGCTGGGTGTCACGTTGAGTTTGGGGACTGCGTGTGCTTCTTCCGCGCTG 3687
 QY 966 GlySerLeuIleValAlaIlySerThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
 Db 3688 TTTCAGATGATCGGAGAGAACGCTTGATTCAGAGGCTTGTGGTCTTCCGATCTAT 3747
 QY 986 AlaLeuThrLeuMetClyMetPheGlnTyrCysValArgGlnSerAlaGlnValGlnAsn 1005
 Db 3748 GCCTTACAGGTGACCTTGATTTGAATGATGATGATGATGATGATGATGATGATGATG 3807
 QY 1006 MetMetIleSerValGlnArgValIleGlyTyrThrAspLeuGlnGlyValAlaProThr 1025
 Db 3808 AATATATAGCCGTGAGAGAGCTCAAGAGTACTTAAAGCGAGACTAGAGCTCCCTCG 3867
 QY 1026 GlnTyrGln---LysArgProProProAlaTyrProHisGlyValIleIlePheAsp 1044
 Db 3868 GTGTTGAGAGAACCGCTGCTCCAGAGGCTGGCCAGAGAGTGGGTGATGAGTTCGG 3927
 QY 1045 AsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuIlyHisIleuThrAlaLeu 1064
 Db 3928 AACTATTCGGTGGGATCCGCGCGCTCCAGTTGCTGTAAGAAATTTGACTCTGCAT 3987
 QY 1065 IleLysSerGlnGlnLysValGlyIleValArgThrGlyAlaGlyLysSerSerLeu 1084
 Db 3988 GTGCAGGTTGGAGAGAGTATGATCGTGGCGCATGCGGCTGGCAAAATCTTCATG 4047
 QY 1085 IleSerAlaLeuPheArgLeuSerGlu---ProGlnGlyLysIleTyrIleAspLysIle 1103
 Db 4048 ACTCTTGGCTATTCGGAATCCGAGAGCGCGAGAGGTGATCTTCATTCAGCGGCTC 4107
 QY 1104 LeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGln 1123
 Db 4108 AATGTGGCACACATTTGGCTCCATGACTGCGTTCAACTCACATCCATCCCTCAGAC 4167
 QY 1124 ProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlnHisThrAsp 1143
 Db 4168 CCATCTCTCTCTCGGCGAGCGCTGCGCATGAACTTGATCCCTTGGCCGTTACTGGAC 4227
 QY 1144 GlnGlnLeuTyrAsnAlaLeuGlnGlnValGlnLeuLysGlnThrIleGlnAspLeuPro 1163
 Db 4228 GAGGACATCTGAGAGACCTGAGACTATCCACCTGATGCAATTGTGAGACAGCCAGCCG 4287
 QY 1164 GlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGlyGlnArgGln 1183

Db 4288 ACAGGCTGATTTTCACTGCTCTGAGGGTGGAGTAATCTCAAGTTGGCCAGAGCGAG 4347
 QY 1184 LeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGlnAla 1203
 Db 4348 CTCGTGTCTTACCCCGAGCCCTGCTCCGAAAGAGCCGTGCTGTTTAAACAGAGCC 4407
 QY 1204 ThrAlaAsnValAspProArgThrAspGlnLeuIleGlnLysLysIleArgGlnLysPhe 1223
 Db 4408 ACCGTGCATTTGACCTGAGACTGATGACCTCATCCAGGGTACCATCCGTTACCGATT 4467
 QY 1224 AlaHisCysThrValLeuThrThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys 1243
 Db 4468 GAAAGCTGACATGTACTGACATCCGCCACCGCTCAACACATCATGATGATCAACCGG 4527
 QY 1244 IleMetValLeuAspSerGlyArgLeuLysGlnTyrAspGlnProTyrValLeuGln 1263
 Db 4528 GTCTGTGCTTGTGACAAAGAGTATGATGATTTGATTTCTCCAGTAAACCTCATTCGA 4587
 QY 1264 AsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlnLysAla 1279
 Db 4588 ---GCTGAGGCACTCTTCTATGAGATGGCCAAAGATGAGAGCTGCGC 4632

Search completed: March 14, 2006, 16:34:37
 Job time : 1959 secs